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OM protein - protein search, using sw model
                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Run on: May 8, 2002, 11:46:20 ; Search time 10.16 Seconds (without alignments) 57.740 Million cell updates/sec

Title: Perfect score: US-09-647-457-2 16

Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 100059 segs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 30 |) (L | 3 2 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | œ | 7 | 0 | ₅ | 4 | ω | N | | Result No. |
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| NO3C_MAT45 | LKHOCA | 3AR_PIG | SCHPO | R36A_SCHPO | RHOPL | FLIQ_TREPA | FLIQ_HELPY | _DICDI | _METJA | PLEWA | ENOL_HUMAN | ENO_SCHMA | ENO_SCHJA | ENO_LOLPE | ENO_XENLA | ENO_HOMGA | RAT | MOUSE | ENOG_HUMAN | 3_RAT | \mathbf{H} | MOUSE | HUMAN | ENOB_CHICK | RAT | ENOA_MOUSE | HUMAN | CHICK | _BOVIN | ANAPL | ALLMI | HUMAN | : |
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RESULT

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| NU6M_PTYAL | NU6M_LATCH | NU6M_FRACR | NU6M_CARAU | NU6M_AETPY | NU6M_CYPCA | LSHB_HORSE | YSAA_ECOLI | YF47_SYNY3 | RL27_PYRST | NU3C_WHEAT | NU3C_ORYSA |
| | 003175 lat | P43201 fra | 078689 cai | P43191 aei | P24982 CY | P08751 equ | P56256 esc | P74662 syr | 002984 руз | P26303 tri | P12126 ory |
| ptychoramph | latimeria c | atercula | rassius a | thia pygm | prinus ca | uus cabal | escherichia | nechocyst | robotrys | iticum ae | yza sativ |

ALIGNMENTS

| Qу | M B Q | SOUR THE |
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| 1 LVVGLCT 7 285 LVVGLCT 291 | Query Match 43.8%; Score 7; DB 1; Length 335; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | HUMAN MPBL_HUMAN MPBL_HUMAN |

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Best Local :
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P19140;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (TAU-
                   Anas platyrhynchos (
Eukaryota; Metazoa;
Archosauria; Aves; )
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  NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÉMBL; L28078; AAA53671.1; -. HSSP; P56252; 1PDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular evidence for the origin Proc. Natl. Acad. Sci. U.S.A. 91:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8496;
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                                                                                                                                                                                                                                                                                                                                                                                              1 LVVGLCT 7
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PATHWAY: GLYCOLYSIS.

SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
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223
271
296
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02; Enolase; 1.
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                                          (Domestic duck).
; Chordata; Crani
                       Neognathae;
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223
271
296
395
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0; Mismatches
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                                      Craniata; Vertebrata; Euteleostomi;
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                     Anseriformes;
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AGNESIUM (BY S
AGNESIUM (BY S
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Y SIMILARITY).
                     Anatidae;
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Best Local
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20-AUG-2001
20-AUG-2001
20-AUG-2001
SEQUENCE FROM N.A. Chapman K.L., Newman Boot-Handford R., Wa
                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
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METAL
SEQUENCE
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOVIN
                                                                                                                                                                   Bovidae; Bovinae;
                                                                                                                                                                                                                                                         Bos taurus (Bovine).
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ACT_SITE
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-i- FUNCTION: BOTH AN ENZYME AND A LEWS STRUCTURAL PROTEIN.
--- CRTALVELO ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENOA_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M20749; AAA49218.1; -. EMBL; X14195; CAA32409.1; -. PIR; A32132; A32132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformat, the European Bioinformatics Institute. They use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See loor send an email to license@isb-sib.ch).
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Probom; PD000902; Enolase; 1.
PROSTIE; PS00164; ENOLASE; 1.
Lyase; Glycolysis; Magnesium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: GLYCOLYSIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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         man B.,
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SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-Kidney;
MEDLINE-9535305; PubMed-7629021;
Tanaka M., Maeda K., Nakashima K.;
"Chicken alpha-enolase but not beta-
"Chicken alpha-enolase but not beta-
                                                                                                                                                                                                                                                                                      _CHICK
_CHICK STANDARD; PRT; 433 AA.
P51913;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Alpha enolase is upregulated in proliferative chondrocytes in epiphyseal growth plate and in human osteoarthritic tissue."; submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                         (PHOSPHOPYRUVATE HYDRATASE).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                              tyrosine-phosphorylation site: cDNA cloning and analysis.";
J. Blochem. 117:554-559(1995).
-I- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                              Archosauria; Aves;
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PATHMAY: GLYCOLYSIS.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IDENTIFIED IN MEMORIAL NOCALIZED IN MUSCLE TISSUE, AND GAMMA ISOUND ONLY IN MERVOUS TISSUE.

SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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 COFACTOR: MAGNESIUM
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Pred. No.
                                                                                                                                                                                                                              Galliformes;
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 FOR CATALYSIS
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=90323004; PubMed=2373081;
MEDLINE=90323004; PubMed=2373081;
Giallongo A., Oliva D., Cali L., Barba G., Barbieri G.,
Giallongo A., Oliva D., Cali L., Barba G., Barbieri G.,
"Structure of the human gene for alpha-enolase.";
"Structure of the human gene for alpha-enolase.";
"Structure of the human gene for alpha-enolase.";
Walter M., Leidenberger F.A., Schweppe K.W., Berg H., Northemann W.; "Autoreactive epitopes within the human alpha-enolase and their recognition by sera from patients with endometriosis.";
                                                  MEDLINE=96422099; PubMed=8824716;
                                                                  TISSUE-Endometrium;
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alpha

enolase."; Acad. Sci.

U.S.A. 83:6741-6745(1986).

Feo s:

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Query Match
Best Local :
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P06733; Q16704; Q9UM55;
Q1-JAN-1988 (Rel. 06, Created)
Q1-APR-1988 (Rel. 07, Last sequence update)
Q1-APR-2001 (Rel. 40, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
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                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
NCBI_TaxID=9606;
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Giallongo A., Feo S., Moore R., Cr
"Molecular cloning and nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000902; Enolase;
PROSITE; PS00164; ENOLASE;
                                          SEQUENCE FROM N.A. MEDLINE=86313654;
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PATHWAY: GYCOLYSIS.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBUNIT: HOMODIMER (BY SIMILARITY).
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          PubMed=3529090;
PubMed=3529090;
R., Croce C.M.,
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Pred. No. 1.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
  roce C.M., Showe L.C.;
sequence of a full-length cDNA for
                                                                                                                                              Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .9;
                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 433;
                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Matches
                                                                                                                                                              METAL
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Aarhus/Ghent-2DPAGE;
Aarhus/Ghent-2DPAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                        SEQUENCE
                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97295306; pubMed=9150948;
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burg
"A two-dimensional gel database of human colon
Electrophoresis 18:605-613(1997).
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mohamad R.M., Hamdan M.Y., Maki A., , "Induced expression of alpha-enolase cell lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Colon carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onyango P., Lubyova B., Gardellin
"Molecular cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 165-433 FROM N.A MEDLINE=98317532; PubMed=9653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 269-280 AND 306-320.
MEDLINE=95307697; PubMed=7787969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 50:187-198(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL; X16288; CAA34360.1; JL; X16289; CAA34360.1; JL; X16299; CAA34360.1; JL; X16290; CAA34360.1; JL; X84907; CAA59331.1; JL; U88968; AAC39333.1; A29170; A29170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMEN. CYTOPLASMIC.
SUBCELULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYME ALPHA IS PRESENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: GLYCOLYSIS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                          PD000902;
pS00164;
    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                        PR00148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                 IPR000941; Enolase.
                                                                                                                   251
433
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA52387.1;
CAA34360.1;
CAA34360.1;
CAA34360.1;
CAA34360.1;
                                                                                                                                                                                                                                                                                                                                                                           enolase;
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                                                                                                                                                                                                                                                                                                        Enolase;
ENOLASE;
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                                                                                                                                                                                                                                                                                Magnesium;
                        43.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1325;
5406;
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NEPHGE.
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MAGNESIUM (BY S
                          Score 7;
Pred. No.
                                                                                                              MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
F -> S (IN REF. 3).
; B2028684C33140B5 CRC64;
                                                                                                                                                                                                                                                                                  Multigene family
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P., Kurzbauer R., Weith A.; analysis of five novel genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Al-Katib A.;
e in differentiated diffuse large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                DB
                          .9
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                                             Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
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proteins.";
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0;
Gaps
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ENOA_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                             RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sulincich S., Hill D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Toyo-oka K., Wang K., Waltz C., Whittaker C., Wilming L.,
RA Wunshaw-Boris A., Yoshida K., Hasegawa Y. Kawati H., Kohtenki S.
                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENOA_MOUSE STANDARD; PRT; 433 AA.

P17182; Q9DCY7;

01-AUG-1990 (Rel. 15, Created)

20-AUG-2001 (Rel. 40, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
                                                                                     between
                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                    Wynshaw-Boris A., Yoshida K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENOI OR ENO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequences mouse brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90301487;
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                                                                                                                                                     SUBCELLULAR LOCATION: CYTOPLASMIC.

TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT 1
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA 1
FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                                                                                                                                                                                               COFACTOR: MAGNESIUM IS
                                                                                                                                                                                                                                            PATHWAY: GLYCOLYSIS. SUBUNIT: HOMODIMER.
                                                                                                                                     SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                 THE DIMER
                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY:
                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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requires a
an email to
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6J; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Res. 18:3638-3638(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2362815;
X., Chalon P., Lelias J.M., Lamande N., Lucas M.,
license agreement (See license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of cDNAs alpha and
                                                                                                                                                                                                                                                                                                                                  2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                               REQUIRED FOR
                                                                                                                                                                                                                                                                                                                                                                 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                           There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                               CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                   mouse
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                http://www.isb-sib.ch/announce/
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                             Usage
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; Murinae; Mus
                                                                                                                                                                                                                                                                                               FOR STABILIZING
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                                  and
                                                                                 EMBL outstation
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RESULT
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Best Local S
Matches 7
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P04764;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-ALPHA ENOLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X52379; CAA36605.1; -. EMBL; AK002336; BAB22021.1; -. PIR; S10246; S10246.
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INIT_MET
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SWISS-2DPAGE; P17182; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:95393; Enol.
                                                                                                                                                                                                                                                                                  Sakimura K., Kushiya E., Obinata M., Takahashi Y.;
"Molecular cloning and the nucleotide sequence of cDNA to
non-neuronal enclase (alpha alpha enclase) of rat brain
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-85242108; PubMed=2989793;
                                      This
                                                                                                                                                                                                      Nucleic Acids [2]
                                                                                                                                                                                                                                  Takahashi
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 LVVGLCT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LVVGLCT 7
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          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                             SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENGLASE ISOENZYMES HAVE BEEN ITISSUE SPECIFICITY: TISSUES. ISOENZYME ALPHA IS PRESENT IN MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENGLASE FAMILY.
                                                                                                                                          PATHWAY: GLYCOLYSIS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                 COFACTOR: MAGNESIUM
                                                                                                                                                                    THE DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                   OR ENO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycolysis; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                            ENOLASE) (NNE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD000902; Enolase; 1.; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00148; ENOLASE.
non-profit
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433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                       Res.
                                                                                                                                                                                                                                                                        13:4365-4378(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.8%;
100.0%;
  institutions
                                                                                                                                                                                IS REQUIRED FOR CATALYSIS AND FOR
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family.
                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C90082CBA8290EB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> P (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
  as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 433
                                                                                                                                                                                                                                                                                                  CDNA to mRNA for
                                                                                                                                                                                                                                                                                      and liver.";
                                                                                                                                                                                   STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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 ENOB_CHICK
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyase; Glycolysis; Magnesium; Multigene family.
INIT_MET 0 0
ACT_SITE 157 157 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A23126; A23126.
HSSP; P56252; 1PDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1988 (Rel. 07, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
(PHOSPHOPYRUVATE HYDRATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X02610; CAA26456.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           (FROGERIA (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordatae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENOB_CHICK P07322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                           analysis.
                                                                                                                                                                                                                                                                                                  "Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence analysis "
                                                                                                                                                                                                                                                                                                                                     MEDLINE=95355305; PubMed=7629021;
Tanaka M., Maeda K., Nakashima K.
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=WHITE LEGHORN; TISSUE=Muscle;
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                                                                   -i- PATHWAY: GLYCOLYSIS.
-i- SUBUNIT: HOMODIMER.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                   Biochem. J. 236:115-126(1986)
                                                                                                                                                                                              enolase.
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                       -!- COFACTOR: MAGNESIUM IS
                                                                                                                                                                                                            Russell G.A., Dunbar B., Fothergill-G
"The complete amino acid sequence of
                                                                                                                                                                                                                          Russell G.A.,
                                                                                                                                                                                                                                       MEDLINE=87075592; PubMed=3539098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 LVVGLCT 389
                                                                                                                                                                  -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                               Biochem. 117:554-559(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LVVGLCT
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                                                                                                                            THE DIMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000902; Enolase; 1. PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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244
292
317
46984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.8%;
                                                                                                                                                                    2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                          Fothergill-Gilmore L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1; Pred. No. 1.9
0; Mismatches
                                                                                                                                        REQUIRED FOR CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
; F1A25F010C276E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433
                                                                                                                                                                                                              chicken skeletal-muscle
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                                                                                                                                           AND FOR STABILIZING
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ENOB_HUMAN
ID ENOB_H
AC P13929
DT 01-JAN
DT 01-OCT
DT 20-AUG
DE ENGS.
OS HOMO S
OC EUKARY
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RX MEDLIN
RA PESHAV
RT "Struc
RT from a
RL Nuclei
RN [2]
RP SEQUEN
RX MEDLIN
RA PESHAV
RT "MO1ec
RT (ENO3)
RL Bioche
RN [3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                           Peshavaria M., Day I.N.M.; "Molecular structure of the human muscle-specific enolase gene (ENO3).";
                                                             SEQUENCE FROM N.A.
MEDLINE=91222137; PubMed=1840492;
                                                                                                                  Peshavaria M., Hinks L.J., Day I.N.M.;
"Structure of human muscle (beta) enolase mRNA and protein deduced from a genomic clone.";
                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 40, Last annotation update)
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
(SKELETAL MUSCLE ENOLASE) (MSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
                                                                                             Nucleic Acids Res. [2]
                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
METAL
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=90067857; PubMed=2587223;
                                                                                                                                                                                                                  ENO3.
Homo sapiens (Human).
Motazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyase; G
INIT_MET
MOD_RES
                                                                                                                                                                                                NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                P13929;
                                                                                                                                                                                                                                                                                                                                            ENOB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00113; enolase; 1 PRINTS; PR00148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D37901; BAA07133.1; -. PIR; A23850; A23850. HSSP; P56252; 1PDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000941; Enolase.
Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                        383 LVVGLCT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LVVGLCT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000902; Enolase; 1.
; PS00164; ENOLASE; 1.
Glycolysis; Magnesium; Multigene family; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
             J. 275:427-433(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                      17:8862-8862(1989)
                                                                                                                                                                                                           Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E -> D (IN REF. 2).

P -> L (IN REF. 2).

M -> V (IN REF. 2).

CK -> SH (IN REF. 2).

G -> D (IN REF. 2).

H -> D (IN REF. 2).

HT -> DP (IN REF. 2).

Y -> L (IN REF. 2).

Y -> L (IN REF. 2).

F -> S (IN REF. 2).

F -> A (IN REF. 2).

G -> A (IN REF. 2).

KT -> EQ (IN REF. 2).

KT -> EQ (IN REF. 2).

KT -> EQ (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACETYLATION.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                         433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                          Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                           Homo.
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SOLD BY A SERVICE 
        В
                                                      Qy
                                                                                                             Matches
                                                                                                                                                           Query Match
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EMBL; X51957; CAA36216.1; -.
EMBL; X55976; CAA39446.1; -.
EMBL; X55976; CAA3946.1; -.
EMBL; X55976; CAA40163.1; -.
EMBL; X5593; S15933.
PIR; S15933; S15933.
PIR; S1693; S1693.
PIR; S1695; S1695.
PIR; S31650; S31650.
PIR; S33330.
S1593; S33330.
                                                                                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                       METAL
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P56252; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000902; Enolase; 1. PROSITE; PS00164; ENOLASE; 1.
383 LVVGLCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 214:36/
-!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Differential splicing in the 5'-untranslated sequence generates forms of mRNA.";
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MEDLINE=90245587; PubMed=2336366;
Cali L., Feo S., Oliva D., Giallongo A.;
"Nucleotide sequence of a cDNA encoding the human muscle-specific encolase (MSE).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                yase; Glycolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93292497; PubMed-8513787;
Giallongo A., Venturella S., Oliva D., Barbieri G., Rubino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural features of the human gene for muscle-specific enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feo S.;
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                                                                                                                                      Local
                                                      1 LVVGLCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT I MOST TISSUE, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA I FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00113; enolase; 1
S; PR00148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P56252; 1PDY.
                                                                                                       Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acids Res. 18:1893-1893(1990).
                                                                                                                                                                                                                                     157
244
292
317
84
161
433 ;
                                                                                                          Conservative
     389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214:367-374(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Magnesium;
                                                                                                                                                                                                                                        46855
                                                                                                                             43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                        ¥
                                                                                                                                                                                                                                                        BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

V -> A (IN REF. 3).

K -> N (IN REF. 1 AND 2).
                                                                                                       0;
                                                                                                                             Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Multigene family.
                                                                                                                                                                                                                                   5F726D743DEBF82F CRC64;
                                                                                                     Mismatches
                                                                                                                             . DB
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                                                                                                                                                      Length 433;
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RESULT

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ID ENOB_MOUSEM
AC P21550
AAC P21550
DT 01-AAC
DT 01-AAC
DT 15-JUL
DE BETA E
GN KELEE
GN KUS MUS MU
OC MAMMMAI
OC EUKARY
OC MAMMMAI
RA LAMMAI
RA LAMMAI
RA LAMMAI
RA Peters
RT Betar
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peterson C.A., Cho M., Rastinejad F., Blau H.M.;
"Beta-enolase is a marker of human myoblast heterogeneity prior to differentiation.";
                                                                                                                                                                                                                                                                                        PIR; S17109;
PIR; A33921;
PIR; S29675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamande N., Brosset S., Keller A., Lucas M., Lazar M.; Submitted (SEP-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1991 (Rel. 18, Created)
01-AIG-1992 (Rel. 23, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 58-433 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/C; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENO3 OR ENO-3.
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                                                                                                                                                                                                                                                                                                                                                                 EMBL; X61600; CAA43797.1; -.
EMBL; X62667; CAA44540.1; -.
EMBL; M20745; AAA37554.1; -.
EMBL; X57747; CAA40913.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamande N., Mazo A.M., Lucas M., Montarras D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Legault-Demare L., Lazar M.;
  INIT_MET
ACT_SITE
                                                                                                                                                                                                             MGD; MGI:95395; Eno3.
                                                                                                                                                                                                                                            SWISS-2DPAGE; P21550; MOUSE.
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                                                                                                                                                                                    InterPro; IPR000941; Enolase.
                                                       Lyase;
                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT I
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA I
FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: GLYCOLYSIS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. 151:626-629(1992).
                                                                                                                                                           PF00113; enolase;
                                                       Glycolysis; Magnesium; Multigene family.
                                                                                                            PD000902;
                                                                                                                                     PR00148; ENOLASE.
                                                                                   PD000902; Enolase; 1. PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                        NOMSB.
A33921.
S29675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433
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Best Local
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METAL
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P25704; Q9N0N6;
01-MAY-1992 (Rel. 22, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
(SKELETAL MUSCLE ENOLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                     directed mutagenesis (E417L) of the gene, expression of the wild-type and mutant genes in Escherichia coli.";
Thesis (1995), Concordia University, Montreal / Quebec, Canada.
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zheng S.-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chin c.c.Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91113295; PubMed=2275753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                         EMBL; AF260259; AAF71925.1; PIR; A37210; A37210. HSSP; P56252; 1PDY.
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The primary structure of rabbit muscle enolase.";
J. Protein Chem. 9:427-432(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 LVVGLCT 389
                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                          InterPro; IPR000941; Enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LVVGLCT 7
                                                                                                                                                                                                                                                                    PATHWAY: GLYCOLYSIS.
SUBGNIT: HOMODIMER.
SUBGOELLLAR LOCATION: CYTOPLASMIC.
SUBCELLLAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT I DENT TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA I FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: MAGNESIUM IS
                                                                                                                                                                                                                                                                                                                                                                             THE DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA cloning of rabbit muscle-specific enolase gene, site
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AG -> NA (
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
AG -> NA (IN REF. 3).
B318B76338ZD3FA8 CRC64;
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PRINTS; PR00148; ENOLASE. ProDom; PD000902; Enolase; PROSITE; PS00164; ENOLASE;

PF00113; enolase;

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                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
               EMBL; Y00979;
                                                                                                                                                                                                                                                                                                                         Sakimura K., Kushiya E., Ohshima-Ichimura Y., Mitsui H., Takahashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-WISTAR;
MEDLINE-89121113; PubMed-2914621;
Takayama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                               FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-27 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                        Ohshima Y., Mitsui H., Takayama
Takahashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
(SKELETAL MUSCLE ENOLASE).
                                                                                                                                                                                                                                                                                          "Structure and expression of rat muscle-specific FEBS Lett. 277:78-82(1990).
                                                                                                                                                                                                                                                                                                                                              MEDLINE=91099531;
                                                                                                                                                                                                                                                                                                                                                                                                "cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta beta enolase).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
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les 7; Conser
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                                                                                                                                 SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT I
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA I
FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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                                                                                                                                                                                                                   PATHWAY: GLYCOLYSIS.
SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                       COFACTOR: MAGNESIUM IS
                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY:
                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
   x57774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
CAA68788.1; -.
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14, Last seq
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100.0%
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MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                          (See http://www.isb-sib.ch/announce/
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                                                     TISSUE-Hematopoietic;
MEDLINE=91257823; PubMed=2045099;
Oliva D., Cali L., Feo S., Giallo
"Complete structure of the human
                                              enolase."
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                               normal and tumor tissues of human origin.";
J. Neurosci. Res. 19:450-456(1988).
                                                                                                                                                                                                                                    "Human gamma enolase: isolation of a cDNA clone and expression
                                                                                                                                                                                                                                                                                    van Obberghen E., Kamholz J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McAleese S.M., Dunbar B., Fothergill J., Hinks L., Day "Complete amino acid sequence of the neurone-specific of enclase (NSE) from human brain and comparison with non-neuronal alpha form (NNE)."!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR 1989 (Rel. 10, Created)
01-MAR 1989 (Rel. 10, Last sequence update)
20-AUG 2001 (Rel. 40, Last annotation update)
GAMMA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                                                                                                                                                                                                                                                                                                           MEDLINE=88259288;
                                                                                                                                                                                                                                                                                                                                                                                                                          enolase.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    Lazzarini R.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90006764; PubMed=2792767;
Oliva D., Barba G., Barbieri G., Giallongo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P09104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
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InterPro; IPR000941; Enolase.
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                  10:157-165(1991).
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                                                                                Giallongo A.;
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Day I.N.M., Allsopp M.T.E.P., Moore D.C.M., Thompson R.J.;
"Sequence conservation in the 3' -untranslated regions of neurone-
specific enclase, lymphokine and protooncogene mRNAs.";
FEBS Lett. 222:139-143(1987).
                                                                                                 CONFLICT
                                                                                                                                                                                                                          Lyase; G
                                                                                                                                                                                                                                                                                                                                        PIR; JU0060; NOHUG.
PIR; S02077; S02077.
PIR; S02616; S02616.
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EMBL; M22349; AAB59554.1; -.
EMBL; M36768; AAA52388.1; ALT_INIT.
EMBL; X51956; CAA36215.1; -.
EMBL; U47924; AAB51320.1; -.
EMBL; X14327; CAA32505.1; -.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-96303695; PubMed-8723724;
                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                               HSSP; P56252; 1PDY.
MIM; 131360; -.
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                                                                                                                                       VARIANT
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TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN ITISSUE SPECIFICITY IN TISSUES. ISOENZYME ALPHA IS PRESENT IN MOST TISSUE, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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Q -> E (IN REF. 2, 4 A)
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RESULT 15
ENOG_MOUSE
Вb
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GAMMA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENOG_MOUSE P17183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequences of cDNAs alpha and mouse brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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Lazar M., Caput D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90301487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENO2 OR ENO-2.
                                                                                                                                                                                     EMBL; AC002397; AAC36002.1; PIR; S10247; S10247.
                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEURAL
SEQUENCE
              METAL
                         METAL
                                                                                          ProDom; PD000902; Enolase; PROSITE; PS00164; ENOLASE;
                                                                                                                      PRINTS;
                                                                                                                                  Pfam;
                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                EMBL; X52380; CAA36606.1; -.
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                                        METAL
                                                     ACT_SITE
                                                                            Lyase; Glycolysis; Magnesium; Multigene family
                                                                                                                                               InterPro;
                                                             NIT_MET
                                                                                                                                                                                                                                                                                                                                                IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: GLYCOLYSIS.
SUBGUIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE DIMER.
                                                                                                                                               MGI:95394; Eno2.
rPro; IPR000941; Enolase.
                                                                                                                                 PF00113; enolase;
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H., Chinault A.C., Belmo
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MAGNUESIUM (BY SIMILARITY).

MAGNUESIUM (BY SIMILARITY).

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Sciurognathi;
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Belmont J.W., 1
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Miller W.,
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Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVGLCT 7
Db 383 LVVGLCT 389

Search completed: May 8, 2002, 11:47:58
Job time: 98 sec
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Maximum DB seq length: 2000000000
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| AAG73945 | AAG20165 | AAY60045 | AAB08264 | AAW88640 | AAB24774 | AAG20166 | AAY59964 | AAR95493 | AAY11445 | AAB29816 | AAW28191 | AAB09384 | AAY87436 | AAW62337 | AAW07465 | AAY92115 | AAR72638 | AAY43201 | AAW00294 | AAY82822 | AAY82821 | AAY20333 | AAU03503 | AAB76807 | AAG90949 | AAB20279 | AAM24149 | AAY43200 | AAW54357 | AAW14001 | AAB42064 | 58 | AAY43192 |
| Human colon cancer | Arabidopsis thalia | Human endometrium | Amino acid sequenc | Secreted protein e | Plant SDF encoded | ۳. | Human endometrium | E21, monoclonal an | 5' EST Se | Human secreted pro | Staphylococcus aur | Hepatitis GB virus | Cationic antimicro | Bactolysin - antim | Antimicrobial cati | Fibroblast growth | Cladosporium herba | Schizophrenic deri | Penicillin V amido | tun | Uroplakin tumour a | Human microtubule | Human protein kina | Corynebacterium gl | C glutamicum prote | Moraxella catarrha | Human EST encoded | Schizophrenic deri | Alpha Enolase. Ho | Enolase protein. | Human ORFX ORF1828 | Breast and ovarian | Schizophrenic deri |

ALIGNMENTS

RESULT AAY43191

سر

Schizophrenic derived antibody binding epitope #1

11-JAN-2000 (first entry)

AAY43191;

AAY43191 standard; peptide; 16

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XXX SOX XXX DE
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                                                                                                                                                                                                                         Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
                                                                                                                                                                                                        Synthetic
This sequence is a peptide of the invention, which binds antibodies found
                   Claim.2; Page 21; 37pp; English.
                                      New peptides useful for diagnosis of schizophrenia
                                                            WPI; 1999-611037/52
                                                                               Shinitzky M,
                                                                                                   (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                        02-APR-1998;
                                                                                                                                            30-MAR-1999;
                                                                                                                                                               14-OCT-1999.
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                                                                                Deckmann M;
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9 qiktgpac 16

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RESULT
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                                                                                                                                                                    Sequence
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Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
                                                                                                                                                          AAY43198;
                                                                 Schizophrenic derived antibody binding epitope #8
                                                                                                                   11-JAN-2000
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          Claim 4; Page 21; 37pp; English
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                              New peptides useful for diagnosis
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Matches Query Match Best Local

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                                                    This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.
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                   Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
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                                                         Schizophrenic derived antibody binding epitope #5
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                                                                                                               AAY43195;
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       Claim 3;
                                                New peptides useful for diagnosis
                                                                                                                                               Shinitzky M,
                                                                                                                                                                                                                                                02-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         do so without having to first isolate the platelet-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.8%; ilarity 100.0%; Conservative
                                                                                                                                                             20
                                                                                                                                                                                                                    (PAA) fraction.
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deckmann
                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98IL-0123925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-IL00190.
                                                 43.8%; Score 7;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; DB 2; Pred. No. 0.6 0; Mismatches
                          0;
                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
b. 0.69;
                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                          0;
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                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                             Indels
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                          Gaps
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RESULT 1
AAXY419
IID AAYY4
XX AAY4
XX Schi
MX Schi
KW Schi
KW Plat
XX Schi
XX 
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XXX XXX XXX
                                                                                                                                                                                                                                                                                                                  RESULT 12
AAY43192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY43199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizophrenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-611037/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shinitzky M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09951725-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 21; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides useful for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies (PAA) fraction.
                     Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
                                                                                                           Schizophrenic derived antibody binding epitope #2.
                                                                                                                                                                                                                                                                                       AAY43192 standard;
                                                                                                                                                                        11-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LVVGLCT 7
||||||
4 lvvglct 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                    12 lvvglct 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LVVGLCT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deckmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98IL-0123925.
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                                                                                                                                                                                                                                                                                    peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                             28
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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AAB58877
ID AAB5
XX AAB5
AC AAB5
XX 27-b
XX Brea
XX Huma
KW Huma
KW moot
KW antij
KW antij
KW addi
KW antij
KW mult
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KW mult
XX DS Home
XX WO2(
YX WO2(
YX WO21-i
YX WO21-i
YX WO3-i
PD 21-i
XX U3-i
PA (HU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                  (HUMA-) HUMAN GENOME SCI INC
                                                                                08-MAR-2000; 2000WO-US05881
                                                                                                                                              WO200055173-A1
                                                                                                                                                                                                                  Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
                                                                                                                                                                                                                                                                  nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
                                                                                                                                                                                                                                                                                                                                           Breast and ovarian cancer associated antigen protein sequence SEQ ID 585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.
                                                  12-MAR-1999;
                                                                                                               21-SEP-2000
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                        cardiovascular disorder; wound healing;
                                                                                                                                                                                                                                                                                                              Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB58877 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides useful for diagnosis of schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinitzky M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 lvvglct 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deckmann
                                               99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  %; Score 7; DB 2
%; Pred. No. 0.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                      neurological disease
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antianaemic; gene therapy; cancer; proliferative disorder; hypertension, neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

immunostimulant; thrombolytic; coagulant; vasotropic; antidiabeti hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; Human ORFX ORF1828 polypeptide sequence SEQ ID NO:3656

08-FEB-2001

(first entry)

vulnerary;

antipsoriatic; antiparkinsonian;

reading frame; ORFX; detection; cytostatic; hepatotropic;

nootropic; neuroprotective;

Human; open

WO200058473-A2 Homo sapiens. allergy; aplabone damage;

contraceptive.

cartilage damage; antiinflammatory disease;

coagulation

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, altergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                                   AAB42064 standard; Protein; 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1022-1023; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF21780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 lvvglct 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LVVGLCT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-611515/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anoxia and epilepsy; and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
b. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT :
                                                                                                                                                                                                                                                                                                                                                                                                                                  cc which represent the human ORFX open reading frames 1 to 3161. The ORFX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; cd antidiabetic; hypotensive; dermatological; immunosuppressive; cc antidiabetic; hypotensive; dermatological; immunosuppressive; cc antidiproid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating cr uncleic acids can be used to express ORFX proteins in gene therapy cc vectors. The proteins and nucleic acids may be used to treat cancers, cr proliferative disorders, neurodegenerative disorders, osteoarthritis, cr prefit vs host disease, cardiovascular disease, diabetes mellitus, ch hypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, cc bacterial or fungal infection, malaria, autoimmune disorders, asthma, cc allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as contraceptive.
δÃ
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 2810-2811; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA,
            JP08308584-A
                                                                                                                                                                                AAW14001;
                                                                                                                                                                                                            AAW14001 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
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                                         Homo sapiens
                                                                        enolase;
                                                                                        PCR;
                                                                                                                   Enolase protein
                                                                                                                                                    23-MAY-1997
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                                                                                                                                                                                                                                                                                           379
                                                                                                                                                                                                                                              15
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                                                                                     polymerase chain reaction; primer; amplify; tyrosine;
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                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
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                                                                        radioisotope;
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99US-0127636.
99US-0127728.
                                                                                                                                                                                                               Protein; 433
                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                   43.8%;
100.0%;
                                                                        antigen
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  Length 429
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                      human; NSE;
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Search completed: May
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                                                                                                                                     Matches
                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                This sequence represents the wild type human enolase (NSE) protein. The primers represented by AAT60282-T60285 were used to amplify tyrosine introduced versions of this sequence. The introduced tyrosine residues combine a radioisotope in such a way as to have no substantial effect or the antigenicity of the protein. The peptides with the introduced tyrosine residue are prepared by expressing a recombinant DNA sequence,
                                                                                                                                                                                                                                        where the tyrosine residue has been introduced via an insertion or
substitution into the wild type sequence. The peptides can then be u
in radioimmunoassays, as the introduction of the label does not alter
the antigenicity of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Introducing tyrosine residues into a protein for radioisotopic labelling - by substitution, addition and/or insertion to a DNA coding for the protein, antigenicity of the protein is unchanged labelling
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10-11; 13pp; Japanese.
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-059703/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EIKE ) EIKEN KAGAKU KK
                                                                      383 lvvglct 389
                                                                                                                                    Local Similarity les 7; Conserv
                                                                                                       1 LVVGLCT 7
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                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                           ,8
2002, 11:44:04; Search time 12.84 Seconds (without alignments) 94.922 Million cell updates/sec
                                                                                                                                      Compugen Ltd.
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Title: Perfect score: Sequence: US-09-647-457-2 90

1 LVVGLCTCQIKTGPAC 16

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | თ | ₅ | 4 | ω | 2 | <u>.</u> | No. | Result | |
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| 49 | 49 | 50 | 51 | 51 | 51 | 51 | 52 | 53 | 55 | 55 | 56 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 65 | 74 | Score | | |
| 54.4 | • | 55.6 | <u>о</u> | 6. | 56.7 | σ. | 7. | 8 | ۳ | 61.1 | | 72.2 | 72.2 | | 72.2 | 72.2 | 72.2 | | ٠ | 72.2 | 72.2 | 72.2 | ٠ | • | 72.2 | | | 82.2 | 1 | Query | dР |
| 446 | 444 | 445 | 446 | 444 | 444 | 326 | 446 | 431 | 433 | 433 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 434 | 433 | 395 | 458 | Length I | | |
| 2 | N | N | N | Ν | 2 | N | N | N | N | | | | | N | 2 | N | N | Ŋ | N | N | N | Ν | Н | 1 | 1 | N | N | N | BB | | |
| S16257 | T12341 | S39203 | T02221 | JQ1187 | JQ1185 | JQ1186 | T03267 | A53665 | S07586 | A23850 | T25040 | A23126 | JC1039 | JC4187 | JC4186 | S06756 | S02072 | A32132 | A29170 | S10247 | S10246 | A24742 | NOXL | NOMSB | NOHUG | A37210 | I50026 | I37360 | ID | | |
| phosphopyruvate hy | probable phosphopy | | | phosphopyruvate hy | 0 | phosphopyruvate hy | | | | | | | | | | | | | | | phosphopyruvate hy | opyruvate | Description | | |

R:Hedges, S.B.

Proc. Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994

A;Title: Molecular evidence for the origin of birds.

A;Reference number: A53470; MUID:94195794

A;Accession: I50026

A;Status: preliminary; nucleic acid sequence not shown; translation not shown; translation in the content of the content

A;Cross-references: GB:L28078; NID:g472796; PIDN:AAA53671.1; PID:g472797

phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment) N;Alternate names: alpha-enolase C;Species: Alligator mississippiensis (American alligator) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 22-Jun-1999 C;Rocession: I50026

RESULT 150026

N

В QΥ

| 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | S | 34 | ω | 32 | 31 | 30 |
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| 43 | Λ 4 3 | 43 | 43 | 44 | 44 | 46 | 46 | 46 | 46.5 | 46.5 | 47 | 47.5 | 47.5 | 48 |
| 47.8 | 47.8 | 47.8 | 47.8 | 48.9 | 48.9 | 51.1 | 51.1 | 51.1 | 51.7 | 51.7 | 52.2 | 52.8 | 52.8 | 53.3 |
| 1338 | 1006 | 456 | 85 | 959 | 43 | 477 | 137 | 125 | 437 | 437 | 446 | 2946 | 1620 | 372 |
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| protein-tyrosine k | soluble vascular e | phosphopyruvate hy | hypothetical prote | MSH1 protein - yea | collagen alpha 1(I | protein enclase F2 | thionin precursor, | alpha-2-thionin - | phosphopyruvate hy | phosphopyruvate hy | phosphopyruvate hy | hypothetical prote | hypothetical prote | phosphopyruvate hy |

ALIGNMENTS

| Query Match 82.2%; Score 74; DB 2; Length 458; Best Local Similarity 87.5%; Pred. No. 0.00053; Matches 14; Conservative 0; Mismatches 2; Indels | N;Alternate names: enclase C;Species: Homo sapiens (man) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 22-Jun-1999 C;Accession: 137360; S22071 B;Verma, M.; Kurl, R.N. Biochem. Int. 30, 293-303, 1993 A;Title: Human lung enclase: cloning and sequencing of cDNA and its inducibility w. A;Reference number: 137360 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Accession: 137360 A;Refsidues: 1-458 <ver> A;Rolecule type: mRNA A;Residues: 1-458 <ver> A;Cross-references: EMBL:X66610; NID:g31178; PIDN:CAA47179.1; PID:g31179 A;Cross-references: EMBL:Data Library, June 1992 C;Function: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to A;Pathway: gluconeogenesis; glycolysis C;Superfamily: enclase C;Superfamily: site: magnesium 2 (Ser) #status predicted F;219,364/Active site: Glu, Lys #status predicted F;254,308,336/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted</ver></ver> | RESULT 1 137360 phosphopyrnyate hydratase (EC 4.2.1.11), lung - human |
|---|---|---|
| æ `: | ext_change 2 f cDNA and i f 2-phospho- colysis; hyd) #status p | |
| 0; Gaps | ts inducit ts inducit p::g31179 p:g1ycerid p-glycerid p-glyase; | |
| 0; |) ility w. ; acid to magnesio | |

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A;Cross-references: GB:X51956; NID:g31164; PIDN:CAA36215.1; PID:g31165
R;McAleese, S.M.; Dunbar, B.; Fothergill, J.E.; Hinks, L.J.; Day, I.N.M.
Eur. J. Biochem. 178, 413-417, 1988
A;Title: Complete amino acid sequence of the neurone-specific gamma isozyme of enolase A;Reference number: S02077; MUID:89091176
A;Accession: S02077
                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M22349; NID:g951199; PIDN:AAB59554.1; R;Oliva, D.; Cali, L.; Feo, S.; Giallongo, A. Genomics 10, 157-165, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: JU0060; MUID:90006764
A;Accession: JU0060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C:Accession: JU0060; S16163; S02077; I56569; S02616; S38303
R:Oliva, D: Barba, G.; Barbieri, G.; Giallongo, A.; Feo, S.
Gene 79, 355-360, 1989
A:Title: Cloning, expression and sequence homologies of cDNA for
A;Molecule type: mRNA
A;Residues: 2-3,'Q',5-239,'M',241-434 <MCA>
A;Cross-references: EMBL:X13120; NID:g31145
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-434 <01
                                                                                                                                                                                                                                                                          A; Accession: S16163
                                                                                                                                                                                                                                                                                        A; Title: Complete structure of the human gene encoding neuron-specific enolase A; Reference number: S16163; MUID:91257823
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A; Residues: 1-434 <OL1>
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C;Keywords: acetylated amino end; carbon-oxygen
F;1/Modified site: acetylated amino end (Ala) #:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: enolase gamma; neuron-specific enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphopyruvate hydratase (EC 4.2.1.11) gamma - human
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C;Keywords: carbon-oxygen lyase; hydro-lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Species: Oryctolagus cuniculus (domestic rabbit)
;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 05-Aug-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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mary structure of rabbit muscle enolase
er: A37210; MUID:91113295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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0.011;
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#status experimental
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A;Pathway: gluconeogenesis; glycolysis
C;Superfamily: enolase
C;Superfamily: enolase
C;Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolyi
F;2-434/Product: phosphopyruvate hydratase gamma #status predicted <MAT>
F;2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #;
F;40/Binding site: magnesium 2 (Ser) #status predicted
F;210,343/Active site: Glu, Lys #status predicted
F;210,343/Active site: Glu, Lys #status predicted
F;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted
                                                                                                                                                                                                                                 N;Alternate names: enclase beta
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
C;Accession: $17109; $18036; $29675; A33921
R;Lamande, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.
submitted to the EMBL Data Library, September 1991
A;Cross-references: EMBL:X61600; NID:g50848; PIDN:CAA43797.1; PID:g50849 R;Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M. submitted to the EMBL Data Library, October 1991
                                                                                                    A; Molecule type: DNA
A; Residues: 1-434 < LAM>
                                                                                                                                                                        A; Reference number: A; Accession: S17109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: A; Note:
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C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:119872; OMIM:131360
A;Map position: 12p13-12p13
A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2;
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Biochim. Biophys. Acta 1158, 120-128, 1993
A;Title: Characterisation of an epitope specific to the neuron-specific isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequence conservation in the 3'-untranslated regions of neurone-specific A;Reference number: S02616; MUID:88005129
A;Accession: S02616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Van Obberghen, E.; Kamholz, J.; Bishop, J.G.
J. Neurosci. Res. 19, 450-456, 1988
A;Title: Human gamma enolase: isolation of a cDNA clone A;Reference number: 156569; MUID:88259288
A;Accession: 156569
                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphopyruvate hydratase (EC 4.2.1.11) beta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: ENO2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in C;Comment: Thr-191 may be important for the enhanced tolerance to chloride ions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 156-173 <HAR>
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A; Residues: 425-434 <DAY>
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A; Residues: 'GC', 29-126, 'N', 128-434 <VAN>
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Pred. No. 0.012;
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N;Alternate names: enclase ENO1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999
C;Accession: S00463
R;Seq911, N: Shrutkowski, A: Dworkin, M.B.; Dworkin-Rastl, E.
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R;Lamande, N.; Mazo, A.M.; Lucas, M.; Montarras, D.; Pinset, C.; Gros, F.; Legault-Demax Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989
A;Title: Murine muscle-specific enolase: cDNA cloning, sequence, and developmental expre A;Reference number: A33921; MUID:89282789
A;Accession: A33921
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A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid A;Pathway: gluconeogenesis; glycolysis C;Superfamily: enolase C;Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; E;40/Binding site: magnesium 2 (Ser) #status predicted E;210,343/Active site: Glu, Lys #status predicted E;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted
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A;Residues: 59-233,'NA',236-434 <LA2>
A;Cross-references: GB:M20745; NID:9193029; PIDN:AAA37554.1; PID:9387144
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A; Residues: 1-434 <LAZ>
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                                                                                                                                                                                                                      A; Gene: ENO1
C; Function:
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-434 <SEG>
                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Enolase isoenzymes in adult and developing Xenopus laevis and characterization A; Reference number: S00463; MUID:88268812 A; Accession: S00463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 251, 31-39, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphopyruvate hydratase (EC 4.2.1.11) ENO1 - African clawed
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Best Local Similarity
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Query Match

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Score 65;

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Length 434;

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A;Cross-references: GB:M11931; NID:g204041; PIDN:AAA41119.1; PID:g204042
R;Sakimura, K.; Kushiya, E.; Takahashi, Y.; Suzuki, Y.
Gene 60, 103-113, 1987
A;Title: The structure and expression of neuron-specific enclase gene.
A;Reference number: PQ0006; MUID:88152493
A;Accession: PQ0006
A;Molecule type: DNA
A;Residues: 1-28 <SA2>
A;Cross-references: GB:M22770; GB:M18742; NID:g205766; PIDN:AAA41725.1; PID:g554480
C;Keywords: carbon-oxygen lyase; gluconecogenesis; glycolysis; hydro-lyase
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A;Title: Molecular cloning and the nucleotide sequence of cDNA for neuron-specific A;Reference number: A24742; MUID:88042683
A;Accession: A24742
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987
C;Accession: A24742; PQ0006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse
N;Alternate names: 2-phosphoglycerate dehydratase; enolase alpha
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999
C;Accession: S10246; A56781
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A; Molecule type: protein
A; Residues: 'X',60,'X',62-67,'X',69-71;'XX',100-109,'X',111-112,'X',114;'X',184-18;
A; Experimental source: peritoneal macrophages
A; Note: sequence modified after extraction from NCBI backbone
C; Superfamily: enolase
C; Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Nucleotide sequences of cDNAs alpha and A;Reference number: S10246; MUID:90301487 A;Accession: S10246
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                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X52379; NID:g55490; PIDN:CAA36605.1; PID:g55491 R;Bottalico, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas, I. Arterioscler. Thromb. 13, 264-275, 1993
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A; Residues: 1-434 <SAK>
                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                A; Reference number: A56781; MUID:93152553
A; Accession: A56781
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                                                                                                                                                                                                                                                              A; Title: Cholesteryl ester loading of mouse peritoneal macrophages
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A; Residues: 1-434 < KAG>
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A;Molecule type: mRNA
A;Residues: 1-434 <GIZ>
A;Cross-references: GB:M14328; NID:g182113; PIDN:AAA52387.1; PID:g182114
A;Cross-references: Translated the codon AAG for residue 193 as His
A;Note: the authors translated the codon AAG for residue 193 as His
R;Walter, M.; Leidenberger, F.A.; Schweppe, K.W.; Berg, H.; Northemann, V
submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X16288; NID:g31172; PIDN:CAA34360.1; PID:g1167843
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989
R;Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Showe, L.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986
A;Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human alpha
A;Reference number: A29170; MUID:86313654
                                                                                                                                                         A; Description: Autoreactive epitopes A; Reference number: S52858
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Eur. J. Biochem. 190, 567-573, 1990
A;Title: Structure of the human gene for alpha-enolase
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C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Jun-2000 C;Accession: S11696; A29170; S52858; A39183
        A;Cross-references: EMBL:X84907; NID:g693932; PIDN:CAA59331.1; PID:g693933
                                      A; Molecule type: mRNA
A; Residues: 1-251, 'S', 253-434 <WAL>
                                                                                              A; Accession: S52858
A; Status: preliminary
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A; Residues: 1-434 <GIA>
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A:Accession: S11696
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C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999
C;Accession: S10247
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Pred. No.
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Pred. No.
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                                                                                                 A;Reference number: S02072; MUID:89121113
A;Action S02072
A; Molecule type: mRNA
A; Residues: 1-434 < OHS>
                                                                                                                                                                                                  R;Ohshima, Y.; Mitsui, H.; Takayama, Y.; Kushiya, E.; Sakimura, K.; Takahashi, FEBS Lett. 242, 425-430, 1989
                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                           C; Accession: S02072
                                                                                                                                                                                                                                                                                                                                          N; Alternate names: enolase beta; enolase, muscle-specific
                                                                                                                                                                                                                                                                                                                                                                        phosphopyruvate hydratase (EC 4.2.1.11) beta - rat
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A;Cross-references: GB:X14195; NID:g62455; PIDN:CAA32409.1; PID:g62456 C;Superfamily: enolase C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-ly.
                                                                                                                                                                                                                                                                                                                                                     R;Wistow, G.J.; Lietman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz, J. Cell Biol. 107, 2729-2736, 1988
A;Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens: A;Reference number: A92750; MUID:89079778
A;Accession: A32132
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C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyas
F;2-434/Product: phosphopyruvate hydratase alpha #status predicted <MAT>
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A;Title: Role of cell-surface lysines in plasminogen binding to cells: identificati A;Reference number: A39183; MUID:91129243
A;Accession: A39183
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A; Residues: 1-434 <WIS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1p36-1p36
A; Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: ENO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 170-182,'I',184,'R',186-190;245-252 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:119871; OMIM:172430
                                                                                                                          Query Match
Best Local :
                                                                                                  Matches
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Best Local Similarity
384 LVVGLCTGQIKTGAPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 LVVGLCTGQIKTGAPC 399
                                                1 LVVGLCTCQIKTGPAC 16
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                                                                                                                          Similarity
                                                                                                  Conservative
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                                                                                                                        72.2%;
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                                                                                                                        Score 65; DB 2;
Pred. No. 0.012;
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                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                             DB 2;
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                                                                                                                                             Length 434
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NID:g57781; is inconsist

PIDN:CAA68788.1; PI tent with that from

PID:g57782 om Fig. 2 i: Fig.

'n

having 40

(beta-)

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A; Introns: 2
C; Superfamil
C; Keywords:
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A; Molecule type: mRNA
A; Residues: 1-84,'A', 86-161,'K',163-434 <CAL>
A; Residues: 1-84,'A', 86-161,'K',163-434 <CAL>
A; Residues: 1-84,'A', 86-161,'K',163-434-88; PIDN:CAA36216.1; PID:g34789
A; Giallongo, A.; Venturella, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.
Eur. J. Biochem. 214, 367-374, 193
A; Title: Structural features of the human gene for muscle-specific enclase. Differential A; Reference number: $33330, MUID:93292497
A; Accession: $33330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 22-Jun-1999
C;Accession: $06756; $14759; $15933; $33330; $08685; $31650
R;Peshavaria, M.; Hinks, L.J.; Day, I.N.M.
Nucleic Acids Res. 17, 8862, 1989
A;Title: Structure of human muscle (beta) enolase mRNA and protein deduced from A;Reference number: $06756; MUID:90067857
A;Accession: $06756
                                   δÃ
                                                                                                                                                                                                                                                        A;Cross-references: GDB:119873; OMIM:131370
A;Map position: 17pter-17p12
A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X55976
R;Call, L.; Feo, S.; Oliva, D.; Giallongo, A.
Nucleic Acids Res. 18, 1893, 1990
A;Title: Nucleotide sequence of a cDNA encoding
A;Reference number: S15933; MUID:90245587
A;Accession: S15933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blochem. J. 275, 427-433, 1991
A;Title: Molecular structure of the human
A;Reference number: S14759; MUID:91222137
A;Accession: S14759
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밁
                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: ENO3
                                                                                                                                                                                                                                                                                                                                                            A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-161, 'K'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Peshavaria, M.; Day, I.N.M.
Biochem. J. 275, 427-433, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphopyruvate hydratase (EC 4.2.1.11) beta - human N;Alternate names: enolase beta; enolase, skeletal m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-434 < PE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X16504; NID: 931169; PIDN: CAA34513.1; PID: 931170
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                                                                                            Matches
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Best Local
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                                          LVVGLCTCQIKTGPAC
                                                                                                                                                                                                             carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1-161, 'K', 163-434 <GIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 81.;
13; Conservative
                                                                                                                Similarity
                                                                                                                                                                                                                                         enolase
                                                                                            Conservative
                                                                                                              72.2%;
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                                                                                                              Score 65; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skeletal muscle; phosphopyruvate hydratase,
                                                                                                                                                                                                                                                             223/1; 289/1;
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0.012;
                                                                                                                DB 2;
0.012;
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                                                                                                                                     Length 434;
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                                                                                                                                                                                                                                                             356/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                muscle-specific enolase (MSE)
                                                                                                                                                                                                                                                           392/3;
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Job time: 102 sec
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-434 <TAN>
A; Residues: 1-434 <TBN>
A; Cross-references: DDBJ: D37901; NID: g974177; PIDN: BAA07133.1; PID: g1616990
C; Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported for tyrosine phosphorylation in Rous sarcoma virus and is important in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Chicken alpha enolase but not beta-enolase has A;Reference number: JC4186; MUID:95355305
A;Accession: JC4187
A;Moleculary A:Moleculary A:Mo
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C;Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all t C;Superfamily: enclase
C;Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein
C;Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein
F;44/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: JC4187
R:Tanaka, M.; Maeda, K.; Nakashima,
J. Biochem. 117, 554-559, 1995
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A;Title: Chicken alpha-enolase but not beta-enolase A;Reference number: JC4186; MUID:95355305
A;Accession: JC4186
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                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: acetylated amino end; carf; 1/Modified site: acetylated amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphopyruvate hydratase (EC 4.2.1.11) beta chain - chicken N;Altcarnate names: beta-2-phospho-D-glycerate hydrolase; enolase C;Species: Gallus gallus (Chicken) C;Date: 14-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
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Best Local S
Matches 13
                                                                                                                                           Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; L/Modified site: acetylated amino end (Met) #status experimental
384
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                                                                              1 LVVGLCTCQIKTGPAC 16
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LVVGLCTGQIKTGAPC
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13; Conser
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Pred. No. 0.012;
0; Mismatches
                                                                                                                                                                                                                Pred. No. 0
                                                                                                                                                                                                                                                          Score 65;
                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                DB 2;
0.012;
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| ALIGNMENTS 6 AA. y binding epitope; diagnosis. \$\square\$\text{\Qb\circ}\$ \text{diagnosis}. . the invention, which | AAW14001 AAW43200 AAW43200 AAW43200 AAW43200 AAW4320166 AAG20166 AAG20166 AAG20166 AAG37552 AAG37552 AAG37551 AAG37551 AAG37551 AAG37551 AAG37566 AAM14627 AAW14627 AAW76070 AAW77591 AAW977592 AAY97593 AAW977593 AAW97759 A |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides useful for diagnosis of schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinitzky M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES & DEV CO LTD
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Pred. No. 0.0002;
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Best Local :
                                 Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
                                                                   Schizophrenic derived antibody binding epitope
                                                                                                                      AAY43198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides useful for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinitzky M,
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93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is a in elevated levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New
                                                                                                                                                                                                                        Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
           Claim 4; Page 21; 37pp; English
                               New peptides useful for diagnosis
                                                                        Shinitzky M,
                                                                                             (YEDA ) YEDA
                                                                                                                  02-APR-1998;
                                                                                                                                       30-MAR-1999;
                                                                                                                                                           14-OCT-1999
                                                                                                                                                                               W09951725-A2
                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                       Schizophrenic
                                                                                                                                                                                                                                                                            11-JAN-2000
                                                                                                                                                                                                                                                                                                 AAY43202;
                                                                                                                                                                                                                                                                                                                     AAY43202 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinitzky M,
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PAA) fraction.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RES & DEV CO LTD
                                                                                                                                                                                                                                                                            (first entry)
                                                                                             RES & DEV CO LTD
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                                                                                                                                                                                                                                                       derived antibody binding epitope #12
                                                                         Deckmann
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                                                                                                                 98IL-0123925.
                                                                                                                                       99WO-IL00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide of the invention, which binds antibodies found in body fluids of schizophrenic patients. The peptide
                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis of schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78;
Pred. No.
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                               schizophrenia
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0.00021;
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QΥ

Matches Query Match Best Local

l Similarity 13; Conser

Conservative

72 81

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Score 65; DB Pred. No. 0.01 0; Mismatches

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RESULT
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 Query Match

Best Local Similarity 81.2

Matches 13; Conservative
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                                    This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated
                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                       platelet-associated antibody; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizophrenic derived antibody; binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizophrenic derived
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                            antibodies
                                                                                                                                                              Claim
                                                                                                                                                                                        New peptides useful for diagnosis of schizophrenia
                                                                                                                                                                                                                                            Shinitzky M,
                                                                                                                                                                                                                                                                                                  02-APR-1998;
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Sequence
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 17
                          (PAA)
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 AA;
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                            fraction
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  schizophrenia;
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RESULT RAY3194
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XX AAY
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DT 11-C
DT 11-C
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AAY43195
ID AAY4
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated
                                                                                                                                      Schizophrenic derived antibody binding epitope #4
                                                         Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
                                                                                                                                                                                                       11-JAN-2000
                                                                                                                                                                                                                                                           AAY43194;
                                                                                                                                                                                                                                                                                                       AAY43194 standard; peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides useful for diagnosis of schizophrenia
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lvvglctgqiktgapc
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Pred. No.
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RESULT
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Claim 3; Page 21; 37pp; English
                       New peptides useful for diagnosis of schizophrenia
                                                                           Shinitzky M,
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                                                                                                                              02-APR-1998;
                                                                                                                                                                                                                                                                  Schizophrenic derived antibody; binding epitope; schizophrenia;
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                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                         platelet-associated antibody;
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                                                                                                     RES & DEV CO LTD
                                                                             Deckmann
                                                                                                                                                                                                                                                                                             derived antibody binding epitope #3
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81.2%;
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                                                                                                                                                                                                                                                         diagnosis
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RESULT 1
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                                                                                                                                                                                        This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides useful for diagnosis of schizophrenia
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                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                          antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasorropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; detection; vulnerary; antipsoriatic; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX ORF1828 polypeptide sequence SEQ ID NO:3656
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                                 proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage contact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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N-PSDB; AAC76273.
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                                                                                                                                        nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 2810-2811; 5507pp; English.
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99US-0127728.
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       cholesterol ester storage, systemic lupus d immunodeficiency (SCID), AIDS, viral,
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                                                                                                                                                                                                                                                                                                       This sequence represents the wild type human enolase (NSE) protein. The primers represented by AAT60282-T66285 were used to amplify tyrosine introduced versions of this sequence. The introduced tyrosine residues combine a radioisotope in such a way as to have no substantial effect on the antigenicity of the protein. The peptides with the introduced where residue are prepared by expressing a recombinant DNA sequence, where the tyrosine residue has been introduced via an insertion or substitution into the wild type sequence. The peptides can then be used in radioimmunoassays, as the introduction of the label does not alter
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Introducing tyrosine residues into a protein for radioisotopic labelling - by substitution, addition and/or insertion to a DN coding for the protein, antigenicity of the protein is unchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 10-11; 13pp; Japanese
                                                                                                                                                                                                                                                                                               the antigenicity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-059703/06.
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                                                                                                                                 Similarity
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                                                                                                         Conservative
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                                                                                                                                                                                                                                          AA;
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                                                                                                                               72.2%;
81.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reaction;
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                                                                                                                                                                                                                                                                                         protein.
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                                                                                                                               Score 65; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65;
Pred. No.
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer; amplify; tyrosine; human; NSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                               DB 18;
0.2;
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).2;
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                                                                                                                                                        Length 433;
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unchanged
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RESULT 13
AAW54357
ID AAW54357
XX AAW543
XX AAW543
AC AAW543
XX Endome
KW Endome
KW 2D gell
XX Homo s
PN WO9810
YX Homo s
PN WO9810
YX O5-SEF
YX O5-SEF
YX O8-APF
PR 06-SEF
XX U8-APF
PR 06-SEF
XX U8-APF
PR 06-SEF
XX U8-APF
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Best Local S
Matches 13
                       WO9951725-A2
                                                                     Synthetic
                                                                                                                                               Schizophrenic derived antibody; binding
                                                                                                                                                                                                  Schizophrenic derived
                                                                                                                                                                                                                                                    11-JAN-2000
                                                                                                                                                                                                                                                                                                       AAY43200
                                                                                                                                                                                                                                                                                                                                                    AAY43200 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins AAW54349-W54364 are examples of proteins produced in the endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need
                                                                                                                          platelet-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 21; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis of hyperplasia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemical markers of human endometrium - useful for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-207057/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383
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                                                                                                                                                                                                                                                                                                                                                                                                       14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lvvglctgqiktgapc 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                  (first entry)
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96GB-0018600
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                                                                                                                                                                                                                                                                                                                                                    peptide;
                                                                                                                     antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.2%;
                                                                                                                                                                                               antibody binding epitope #10.
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Pred. No. 0
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                                                                                                                     diagnosis
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0.2;
                                                                                                                                             epitope; schizophrenia;
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RESULT 1
AAY43203
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                            New
                                                                                    WPI;
                                                                                                            Shinitzky M,
                                                                                                                                                            02-APR-1998;
                                                                                                                                                                                    30-MAR-1999;
                                                                                                                                                                                                                                     W09951725-A2
                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                   Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                       Schizophrenic
                                                                                                                                                                                                                                                                                                                                               11-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                        AAY43203;
                                                                                                                                                                                                                                                                                                                                                                                               AAY43203 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibodies (PAA) fraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 21; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides useful for diagnosis of schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shinitzky M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1999
This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide
                                  Claim 4; Page 21; 37pp; English.
                                                                                                                                   (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                           14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VVGLCTCQIKTGPAC 16
                                                            peptides useful for diagnosis of schizophrenia
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                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deckmann
                                                                                                            Deckmann M;
                                                                                                                                                                                                                                                                                                                       derived antibody binding epitope #13.
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                                                                                                                                                            98IL-0123925.
                                                                                                                                                                                    99WO-IL00190.
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Pred. No. 0.042;
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                                                                     Matches
                                                                                                   Query Match
                                                                                                                                                                                         is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated
                                                                                                                                               Sequence
                                                                                                                                                                                antibodies (PAA) fraction.
                                                                   Local Similarity
nes 12; Conserv
1 lyvglctgqiktg 13
                                      1 LVVGLCTCQIKTG
                                                                                                                                                 15 AA;
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                                      13
                                                                                    64.4%;
92.3%;
                                                                                    Score 58;
Pred. No.
                                                                       Mismatches
                                                                                    DB
0.1;
                                                                                                    20;
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Search completed: May 8, 2002, 11:45:08 Job time: 209 sec

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Minimum
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Copyright (c) 1993 - 2000 Com
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Q9W6D2
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                             Q9W7L2
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                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parameters:
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                                             Q9ng67 tomocerus s
Q9ptx6 lampetra re
Q9ptx5 lampetra re
Q9u5f7 eptatretus
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Q9bt62 homo sapien
Q9bt63 pelusios su
Q9w6d3 pelusios su
Q9w6d2 trachemys s
Q9w6d1 eumeces ine
Q9w6d1 eumeces opendon p
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Q9ng70 peripatus s
                                                                                                                                                                                          Description
                                     096656 penaeus mon
       Q9w712 sceloporus
Q9w711 trachemys s
Q9w710 python regi
                                                       7 tomocerus s

1 tomocerus s
python recalligator
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| 5 | 44 | Ü | 2 | Ξ | Ö | 39 | 8 | 37 | 36 | 5 | 4 | ü | 32 | 3 | õ | 9 | 8 | 27 | 8 | 5 | 24 | S | 2 | 21 | õ |
|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|---------|--------------------|--------------------|--------|---------|--------------------|
| 5 31.2 | 5 31.2 | 5 31.2 | 5 31.2 | 5 31.2 | 5 31.2 | 5 31.2 | 31. | 31. | 31. | 31. | 5 31.2 | 31. | 31. | 5 31.2 | 5 31.2 | 5 31.2 | 6 37.5 | | | | 6 37.5 | | 6 37.5 | 6 37.5 | 6 37.5 |
| 88 | 85 | 81 | 80 | 79 | 74 | 73 | 72 | 71 | 63 | 58 | 56 | 55 | 43 | 36 | 34 | 33 | 2137 | 1242 | 1242 | 727 | 602 | 517 | 230 | 82 | 81 |
| N | 1 | 13 | æ | 4 | N | 12 | 9 | 12 | 4 | 4 | 10 | σ | 13 | N | ω | σ | 4 | 12 | 12 | 10 | 12 | 10 | N | u | ري. |
| Q9KMK7 | 026173 | Q9PVS5 | 047957 | Q9H493 | Q99QR4 | Q98181 | 080086 | Q84043 | 060770 | Q9P0Z4 | Q9MB34 | P81902 | Q9PW52 | Q9A5R6 | Q9URB2 | Q9TSD2 | 015021 | Q9PZW6 | Q9PZW7 | Q9SVH3 | Q9QPU9 | Q9SAD9 | Q9EXH5 | Q9U6U0 | Q9Y0A9 |
| Q9kmk7 vibrio chol | O26173 methanobact | Q9pvs5 oryzias lat | 047957 phoxinus eo | | Q99qr4 streptomyce | Q98181 molluscum c | 080086 bacteriopha | Q84043 influenza a | 060770 homo sapien | Q9p0z4 homo sapien | Q9mb34 phaseolus v | P81902 bombyx mori | Q9pw52 poecilia re | Q9a5r6 caulobacter | Q9urb2 candida alb | Q9tsd2 bos taurus | O15021 homo sapien | | Q9pzw7 eastern equ | arabido | Q9qpu9 bovine herp | Q9sad9 arabidopsis | Ωı | mytilus | Q9y0a9 mytilus gal |

ALIGNMENTS

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SOTE THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                        Q9NPL4

Q9NPL4;

Q9NPL4;

Q9NPL4;

01-OCT-2000 (TremBLrel. 15, Created) 

O1-OCT-2000 (TremBLrel. 15, Last sequence update)

O1-JUN-2001 (TremBLrel. 17, Last annotation update)

ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Auffray C., Ansorge W., Ballabio A., Estivill Lehrach H., Poustka A., Lundeberg J.; "The European IMAGE consortium for integrated human gene transcripts."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Andreu N., Estivill X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                           Glycolysis; Lyase; Magnesium.
NON_TER 1 1
                                                                                                                            PRINTS; PR00148; ENOLASE. ProDom; PD000902; Enolase
                                                                                                                                                                                          InterPro; IPR000941; Enolase.
Pfam; PF00113; enolase; 1.
                                                                                             PROSITE; PS00164; ENOLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
154 AA;
                                                                                                                            Enolase;
16937 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ
Y: 2-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ballabio A., Estivill X., Gibson
Lundeberg J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escarceller M., Sumoy the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
347B95809B1C864D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L.;
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular analysis
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Best Local Similarity
""+" 7; Conserv
     RRR OCC OCE DET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                              O9NG71 PRELIMINARY; PRT; 251 AA.
Q9NG71;
Q9NG71;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00148; ENULAGE: 1. PROSITE; PS00164; ENOLASE; 1. PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H(2)O.

-I-COPACTOR: MAGNESIUM IS REQUIRED FOR THE DIMER (BY SIMILARITY).

-I-PATHWAY: GLYCOLYSIS.

-I-SUBURIT: HOMODIMER (BY SIMILARITY).

-I-SUBCELLULAR LOCATION: CYTOPLASMIC (INCOMINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4-2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
Peripatus sp. 'Peri'.
Peripatus sp. 'Peri'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NG70;
SEQUENCE FROM N.A. STRAIN=LPO156_406;
                                                                                                 Limulus polyphemus (Atlantic horseshoe crab). Eukaryota; Metazoa; Arthropoda; Chelicerata; Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Enolase as a phylogenetic marker.";
"Enolase as a phylogenetic marker.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ
-I- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00113; enolase; 1. PRINTS; PR00148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF258667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PER3248_407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 LVVGLCT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 LVVGLCT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LVVGLCT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LVVGLCT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF72638.1; -.
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17582 MW;
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100.0%;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7; DB 5; Pred. No. 4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        840E266ACD36D3CD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB . 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
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                                                                                                                          Merostomata;
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= PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT
Q99KT7
ID Q9
AC Q1
DT 0
DT 0
DT 0
DT 0
OC I
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Q9BT62
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Best Local :
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                     099KT7;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
SIMILAR TO ENOLASE 1, ALPHA
                                                                                                                                                                                                                                                                                                                                                             Q9BT62;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
01-JUN-2001 (TrEMBLrel. 37, 1629132) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q99KT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00148; ENOLASE.
PRODOM; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regier J.C., Shultz J.W.;
"Enclase as a phylogenetic marker.";
"bnolase as a phylogenetic marker.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOI
   Eukaryota;
            Mus musculus (Mouse)
                                                                                                                                                                                                                                         EMBL; BC004325; AAH04325.1;
NON_TER 1 1
                                                                                                                                                                                                                                                                         Strausberg
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                  UNKNOWN (PROTEIN FOR IMAGE:3629132) (FRAGMENT). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BT62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY:
EMBL; AF258666;
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                     TISSUE=CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycolysis; Lyase; Magnesium
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                  222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 LVVGLCT 236
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity nes 7; Conserv
                                                                                                                                                       1 LVVGLCT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LVVGLCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H(2)0.
                                                                                                                                  LVVGLCT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000941; Enolase.
                                                                                                                                                                                                                                                              (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                272
  Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                            PRELIMINARY;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO THE ENOLASE AAF72637.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
27452 MW;
                                                                                                                                                                                                                                29883 MW;
   Chordata;
                                                                                                                                                                                                                                                                                                                               Primates;
                                                                                                                                                                                      43.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.8%;
                               17, Created)
17, Last sequence update)
17, Last annotation updat
                       NON-NEURON
                                                                                                                                                                           0;
                                                                                                                                                                                     Score 7;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7;
Pred. No.
   Craniata;
                                                                                                                                                                                                                                                                                                                               Catarrhini;
                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                08F1755ADEA88D0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEE7B1BA7A87693F CRC64;
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                      No.
                                                                            353
                                                                                                                                                                                                                                                                                                                                                                                                                   272
                                                                                                                                                                                      DB 4;
), 6.1;
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                       (FRAGMENT).
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  Vertebrata;
                                                                            A
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                                                                                                                                                                                                                                                                                                                               Hominidae;
                                update)
                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                              Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                               Homo
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SO REP
RESULT
Q9W6D2
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Best Local S
Matches 7
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Best Local
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.3.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W6D3;
                                                                                                                                  METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC004017; AAH04017.1; ...
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                     Hedges S.B., Poling L.L.;
"A molecular phylogeny of reptiles.";
Science 283:998-1001(1999).
                                                                                                                                                                                 PROSITE; PS00164; ENOLASE; 1. Glycolysis; Lyase; Magnesium.
                                                                                                                                                                                          PRINTS; PR0014B; ENOLASE.

ProDom; PD000902; Enolase; 1.

PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                    -i - SIMILARITY: TO THE ENOLASE EMBL; AF115859; AAD20346.1; -. HSSP, P56252; 1PDZ.
InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-99141276; PubMed-9974396;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pelusios subniger.
Eukaryota; Metazoa; Chordata;
Testudines; Pleurodira; Pelome
                                                                                                                                                                                                                             Pfam; PF00113; enolase;
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                                                                                                                                                       ACT_SITE
                                       365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LAAGLCI
                                                           1 LVVGLCT 7
                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (
SIMILARITY: TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                       COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS
                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                  THE DIMER (BY SIMILARITY). PATHWAY: GLYCOLYSIS.
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                                       LVVGLCT 371
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                                                                               similarity
7; Conser
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373
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                                                                                                                                                       373
322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                  AA;
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322
334
40259
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                                                                                          100.0%;
                                                                                                    43.8%;
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                                                                                                                                  MW;
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Pred. No.
                                                                                                                                 BY SIMILARITY.
MAGNESIUM (BY SIMILARITY).
; 399B5C8BB467BD04 CRC64;
                                                                                          Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373
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). 7.5;
                                                                                                                                                                                                                                                                              (BY SIMILARITY)
                                                                                          DB 13;
. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pelusios.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata;
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                                                                                                    Length 373;
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RESULT
Q9W6D1
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Best Local
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NON_TER
ACT_SITE
METAL
SEQUENCE
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.1) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-
                                                                                                                                                                                                 Q9W6D1; PRELIMINARY; PRT; 373 AA.
Q9W6D1; O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hedges S.B., Poling L.L.;
"A molecular phylogeny of reptiles.";
Science 283:998-1001(1999).
-!- CAPALYTIC ACTIVITY: 2-PHOSPHO-D-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCERATE HYDRO-LYASE) (FRAGMENT).
Trachemys scripta (Red eared slider turtle) (Pseudemys scripta).
Eukaryota; Metazoa; (Dordata; Craniata; Vertebrata; Euteleostomi;
Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000941; Enolase.
Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: GLYCOLYSIS.

!- SUBURNIT: HOMODIMER (BY SIMILARITY).

-!- SUBCELLDLAR LOCATION: CYTOPLASMIC (

-!- SIMILARITY: TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9W6D2;
                                     Hedges S.B., Poling L.L.;
"A molecular phylogeny of reptiles.";
Science 283:998-1001(1999).
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-G
                                                                                                                                                                       Eumeces inexpectatus (southeastern five-lined skink).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycolysis; Lyase; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000902; Enolase; 1. PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF115858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99141276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=34903;
                                                                                          SEQUENCE FROM N.A.
MEDLINE=99141276; PubMed=9974396;
                                                                                                                                  NCBI_TaxID=38930;
                                                                                                                                                 Scincidae; Eumeces.
                                                                                                                                                           Lepidosauria; Squamata;
                                                                                                                                                                                                                                                                                                                                                   365 LVVGLCT
                                                                                                                                                                                                                                                                                                                                                                             1 LVVGLCT
H(2)O.
COFACTOR:
THE DIMER
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322
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373
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                                                                                                                                                                                                                                                                                                                                                     371
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 MAGNESIUM IS REQUIRED (BY SIMILARITY).
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322
334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40272
                                                                                                                                                           rdata; Craniata; Vertebrata; Euteleostom Scleroglossa; Scincomorpha; Scincoidea;
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                                        2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +
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MAGNESIUM (BY SIMILARITY).
, 055BBFAF4D64BF99 CRC64;
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               CATALYSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 373;
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                AND
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                STABILIZING
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RESULT
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DT 01
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Matches 7
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Best Local
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    01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2001 (TrEMBLrel. 17,
                                  Q9W6C9;
                                            Q9W6C9
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01-NOV-1999 (TREMBLIEL 12,
01-JUN-2001 (TREMBLIEL 17,
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Science 283:998-1001(1999).
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99141276; PubMed=9974396;
                                                                                                                                                                                                                                                                                                                                                       Sphenodon punctatus (Hatteria) (Tuatara).
Eukaryota; Metazoa; Chordata; Craniata; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
ACT_SITE
METAL
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                    Lepidosauria; Rhynchocephalia; Sphenodontidae; Sphenodon NCBI_TaxID=8508;
                                                                                                                                                                                                               ProDom; PD000902; Enolase; 1.
                                                                                                                                                                                                                           PRINTS; PR00148; ENOLASE.
                                                                                                                                                                                                                                             InterPro; IPR000941; Enolase
                                                                                                                                                                                                                                                        HSSP; P56252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: GLYCOLYSIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: TO THE ENOLASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
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                                                                                           LVVGLCT 371
                                                                                                                                                                                                                                    PF00113; enolase;
                                                                                                                                                                                                                                                               AF115856; AAD20343.1; -.
                                                                                                                                   Similarity 7; Conserv
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373 AA;
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322
334
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                                            PRELIMINARY;
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ENOLASE; 1.
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322
334
40398
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Pred. No.
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Pred. No.
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MAGNESIUM (BY SIMILARITY).
5D46A0D51F63982A CRC64;
                                            PRT;
                                                                                                                                   Mismatches
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                                            373
                                                                                                                                                                                                                                                                                                                                                                                                                           373
                                                                                                                                           DB 13;
5. 7.8;
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     update)
                                                                                                                                                     Length 373;
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                                                                                                                                   Indels
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Best Local :
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Q9NG67;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
Tomocerus sp. 'Tom'.
Tomocerus sp. 'Tom'.
           -!- PATHWAY: GLYCOLYSIS.
-!- SUBUNLT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (
-!- SIMILARITY: TO THE ENGLASE FAMILY.
EMBL; AF258670; AAF72641.1; -.
                                                                                                                                 "Enclase as a phylogenetic marker."; Submitted (APR-2000) to the EMBL/Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
ACT_SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0148; ENOLASE.
ProDom; PD000902; EnoLase; 1.
PROSITE; PS00164; ENOLASE; 1.
Glycolysis; Lyase; Magnesium.
NON_TER
                                                                                          -
                                                                                                                                                        STRAIN=TOM23_406;
Regier J.C., Shultz J.W.;
                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Collembola; Arthropleona; Entomobryoldea; Tomoceridae; Tomocerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE LIBERT (- PATHWAY: GLYCOLYSIS.
-!- PATHWAY: GLYCOLYSIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hedges S.B., Poling L.L.; "A molecular phylogeny of reptiles."; Science 283:998-1001(1999).
                                                                                                                    -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                              Q9NG67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF115855; AAL
HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).

Caiman crocodilus (Spectacled caiman) (Caiman sclerops).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00113; enolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99141276; PubMed=9974396;
                                                                                                                                                                                                              NCBI_TaxID=111305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                            365 LVVGLCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LVVGLCT 7
                                                                                         COFACTOR: MAGNESIUM IS REQUIRED
                                                                             THE DIMER (BY SIMILARITY).
                                                                                                         H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE DIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000941; Enolase
 IPR000941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373
322
334
373 AA;
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crocodyl'idae; Alligatorinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD20342.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO THE ENOLASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40396
                                                                                                                   to the EMBL/GenBank/DDBJ
TY: 2-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
MAGNESIUM (BY SIMILARITY).
, 9F9020B86F66657A CRC64;
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                          FOR
                                                                                                                                                                                                                                                                                                                                             383
                                      (BY
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                                                                                          CATALYSIS
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                                      SIMILARITY)
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                                                                                                                   = PHOSPHOENOLPYRUVATE +
                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 373;
                                                                                          AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT
OF PTX6
AC Q9PTX6
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                                        RESULT
Q9PTX5
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DI
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PTX6 PRELIMINARY; PRT; 394 AA.
Q9PTX6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENGLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
Q9PTX5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE DIMEN NO. 1- PATHWAY: GLYCOLYSIS.
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Glycolysis; Lyase; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0148; ENOLASE.
PRODOM; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- SIMILARITY: TO THE ENOLASE FAMILY EMBL; AB025329; BAA88482.1; -. HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes.";
J. Mol. Evol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20063780; PubMed=10594174;
Kuraku S., Hoshiyama D., Katoh K., S
Monophyly of lampreys and hagfishes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Petromyzontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lampetra reissneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycolysis; Lyase; Magnesium. NON_TER 1 1
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PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000941; Enolase.
Pfam; PF00113; enolase; 1.
                                                                                                                                     345 LVVGLCT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363
                                                                  13
                                                                                                                                                                                  1 LVVGLCT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVVGLCT 369
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S; PR00148; ENOLASE.
                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                          394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49:729-735(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Petromyzontidae; Lampetra.
                                                                                                                                                                                                                                                                                                                                          42583 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41326 MW;
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                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                       43.8%;
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                                                                                                                                                                                                                          Score 7; DB 1; Pred. No. 8.1
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                          BC585FE6C712A3D2 CRC64;
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es supported by nuclear
                     395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                    DB 13;
b. 8.1;
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                     AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 383
                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                       Length 394;
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                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR STABILIZING
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RESULT
Q9U5F7
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Best Local
                                                                                                                                                                                                                                          Q9U5F7 PRELIMINARY; PRT; 395 AA.
Q9U5F7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (Z-PHOSPHOGLYCERATE DEHYDRATASE)
ENOLASE (EC 4.2.1.11) (Z-PHOSPHOGLYCERATE DEHYDRATASE)
GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes.";
J. Mol. Evol. '
-!- CATALYTIC !
                                                                               genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 H(2)0.

-i- COFACTOR: MAGNESIUM IS REQUIRED
THE DIMER (BY SIMILARITY).

-i- PATHWAY: GLYCOLYSIS.
-i- PATHWAY: GLYCOLYSIS.
                                                                                                           MEDLINE=20063780; PubMed=10594174;
Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
"Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
                                                                                                                                                                                           Eptatretus burgeri (Inshore hagfish).
Eukaryota; Metazoa; Chordata; Craniata;
Myxinidae; Eptatretinae; Eptatretus.
NCBI_TaxID-7764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycolysis; Lyase; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB025330; BAA88483.1; HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H(2)O.

H(2)O.

ICAGCIOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).

PATHWAY: GLYCOLYSIS.

I PATHWAY: HOMODIMER (BY SIMILARITY).

SUBCULLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

SIMILARITY: TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=20063780; PubMed=10594174;
Kuraku S., Hoshlyama D., Katoh K., Su
"Monophyly of lampreys and hagfishes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENOLASE-2
                                                                                                                                                        TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000941; Enolase. Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petromyzontiformes; Petromyzontidae; Lampetra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lampetra reissneri.
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         345 LVVGLCT 351
                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LVVGLCT
                                                                    Mol. Evol. CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                  49:729-735(1999).
ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49:729-735(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%;
100.0%;
(BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8591D68662DA8544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suga H.,
                                          FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uga H., Miyata
supported by m
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8
                                          CATALYSIS
                                                                                                                                                                                                                      Hyperotreti; Myxiniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nuclear DNA-coded
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Η.,
                                          FOR STABILIZING
                                                                                                                                                                                                                                                                (2-PHOSPHO-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.8%; Score 7; DB Best Local Similarity 100.0%; Pred. No. 8. Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

TISSUB-ABDOMINAL MUSCLES;
BOONCHOUY C., BOONYAWAN B., Panyim S., Sonthayanon B.;
BOONCHOUY C., BOONYAWAN B., Panyim S., Sonthayanon B.;
"Complete cDNA sequence of phosphopyruvate hydratase (enolase) from marine shrimp, Penaeus monodon.";
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.

-I- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O96656 PRELIMINARY; PRT; 434 AA.
O96656;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
                                                                                                                                Glycolysis; Lyase; Magnesium; Pyruvate.
ACT_SITE 343 343 BY SIMILARITY.
METAL 355 355 MAGNESIUM (BY SIMILARITY).
SEQUENCE 434 AA; 47265 MW; EB575C6FB541ABD3 CRC64;
                                                                                                                                                                                               PRINTS; PR00148; ENOLASE.
PRODOM; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                             EMBL; AF100985; AAC78141.1; -
HSSP; P50252; IPDZ.
InterPro; IPR009941; Enolase.
Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                    H(2)0.

-I- COPACTOR: MAGNESIUM IS REQUIRED FOR THE DIMER (BY SIMILARITY).

-I- PATHWAY: GLYCOLYSIS.

-I- SUBUNIT: HOMODIMER (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (

-I- SIMILARITY: TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penaeus monodon (Penoeid shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: TO THE ENCLASE FAMILY.
EMBL; AB025326; BAA88479.1; -.
HSSP; P56252; 1PDZ.
InterPro; IPR000941; Enclase.
Pfam; PF00113; enclase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LVVGLCT 7
|||||||
345 LVVGLCT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycolysis; Lyase; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0148; ENOLASE.
PRODOM; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penaeidae; Penaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 395 AA; 43131 MW;
1111111
386 LVVGLCT 392
                                                          Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                              1 LVVGLCT 7
                                                            Conservative
                                                                                                                                                                                                                                                                                         AAC78141.1; -.
                                                                          43.8%;
100.0%;
                                                                          Score 7; ; Pred. No.
                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D351C6700DDC75CD CRC64;
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                FOR CATALYSIS AND FOR STABILIZING
                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
b. 8.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                       Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHOENOLPYRUVATE +
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Search completed: May 8, 2002, 11:48:28 Job time: 113 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                  sp_rodent:*
sp_virus:*.
sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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3 Q9W7L1
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Q9BT62
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O9np14 homo sapien
Q9ng70 peripatus s
Q9bt62 homo sapien
Q99kt7 mus musculu
Q9ng67 tomocerus s
Q9ptx6 lampetra re
Q9ptx5 lampetra re
Q9ptx5 lampetra re
Q9u5f7 eptatretus
O96656 penaeus mon
Q9w712 sceloporus
Q9w712 trachemys s
Q9w710 python regi
Q9w710 python regi
Q9pvx2 allilyator m
Q9ng71 limulus pol
Q9ng71 limulus pol
Q9ng73 eumesocampa
Q9ng78 scolopendra
Q4100 dorsophila
Q44101 dorsophila
                                                                                                                                                                       Description
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| 45 | 44 | | | | | | | 37 | | | | 33 | | | 30 | 29 | 28 | 27 | 26 | 25 | 24 | | 22 | | 20 |
|-------------------|--------------------|--------|--------------------|--------|--------------------|--------|--------------------|--------|--------|--------|--------------------|--------------------|----------------------|-------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------------------|--------|--------------------|-------------------|--------------------|
| 43 | 43 | 43 | 44 | 44 | 44 | 45 | 45 | 45 | 45.5 | 45.5 | 46 | 46 | 46 | 47 | 47 | 47 | 47.5 | 47.5 | 48 | 48 | 49 | 51 | 51 | 53 | 53 |
| 47.8 | 47.8 | | 48.9 | 48.9 | | | 50.0 | 50.0 | • | 50.6 | | 51.1 | • | • | • | 52.2 | | | | 53.3 | 54.4 | 56.7 | 56.7 | 58.9 | 58.9 |
| 444 | 429 | 85 | 678 | 427 | 43 | 396 | 234 | 90 | 318 | 317 | 477 | 137 | 137 | 446 | 439 | 429 | 2946 | 1664 | 385 | 162 | 444 | 444 | 326 | 444 | 433 |
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| Q9UAE6 | Q9NDH8 | 007207 | Q9Y6P2 | Q9H152 | Q99225 | Q9YK89 | Q9ATJ6 | Q9S6Y2 | Q98UK2 | Q9W6B0 | Q9C9C4 | Q9S9D7 | Q9T0P1 | Q9UAL5 | Q9U615 | Q9N997 | Q18857 | Q9TVQ2 | Q9NG69 | Q9NG64 | Q9LEE0 | Q9M434 | Q42887 | Q9BPL7 | 093873 |
| Q9uae6 toxoplasma | Q9ndh8 trypanosoma | mycol | Q9y6p2 homo sapien | homo | Q99225 homo sapien | 9 | Q9atj6 arabidopsis | | | _ | Q9c9c4 arabidopsis | Q9s9d7 hordeum vul | . Q9t0p1 triticum ae | Q9ual5 plasmodium | Q9u615 mastigamoeb | Q9n997 leishmania | Q18857 caenorhabdi | | | n | Q91ee0 spinacia ol | _ | Q42887 lycopersico | Q9bpl7 toxoplasma | 093873 pneumocysti |

ALIGNMENTS

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RESULT Q9 NG70 P NG70 Q9 NG70 Q9 NG70 Q9 DT Q9 NG70 Q9 DT Q9 Q9
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Q9BT62
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Best Local (
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Best Local
                                                                                                                                                                                                                                                             Q9BT62 PRELIMINARY; PRT; 272 AA. Q9BT62; Q1-JUN-2001 (TrEMBLrel. 17, Created) O1-JUN-2001 (TrEMBLrel. 17, Last sequence update) O1-JUN-2001 (TrEMBLrel. 17, Last annotation updatunknown (PROTEIN FOR IMAGE: 3629132) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00148; ENOLASE.
ProDom; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
Glycolysis; Lyase; Magnesium.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H(2)0.
"-!- COFACTOR: MAGNESIUM IS REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NG70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regier J.C., Shultz J.W.;
"Enolase as a phylogenetic marker.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHO)
                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EI- SIMILARITY: TO THE ENOLASE FAMILY EMBL; AF258667; AAF72638.1; -
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Peripatus sp. 'Per3'.

Peripatus sp. 'Per3'.

Peripatidae; Peripatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT 2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-
Strausberg
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000941; Enolase. Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: GLYCOLYSIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY)
                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PER3248_407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=126380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104
                                           [SSUE=CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
17582 MW;
                                                                                                                                                                             Primates;
                                                                                                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.2%;
81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 5; Pred. No. 0.00063;
                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840E266ACD36D3CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYSIS
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                                                                                                                                                                          Hominidae;
                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 154;
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                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                             Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Q99KT7
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Best Local S
Matches 13
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Best Local Similarity
                                                                                                                                                                                  ENOLASE (EC. TOMOSENT).

GLYCERATE HYDRO-LYASE) (FRAGMENT).

Tomocerus sp. 'Tom'.

Tomocerus sp. 'Tom'.

Enkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;

Eukaryota; Metazoa; Arthropoda; Tomoceridae; Tomocerus.
                                                                                                                                                                                                                                     Q9NG67 PRELIMINARY; PRT; 383 AA.
Q9NG67;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
                                                                       <del>:</del>
                                                                                           STRAIN-TOM23_406;
Regier J.C., Shultz J.W.;
"Enclase as a phylogenetic marker.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         099KT7;
01-JUN-2001 (TremBLrel. 17,
01-JUN-2001 (TremBLrel. 17,
01-JUN-2001 (TremBLrel. 17,
SIMILAR TO ENCLASE 1, ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004325; AAH04325.1; -.
NON_TER 1 1 1 1
SEQUENCE 272 AA; 29883 MW; 08F1755ADEA88DOC CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                         1 LVVGLCTCQIKTGPAC
          PATHWAY: GLYCOLYSIS.
SUBURIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (
SIMILARITY: TO THE ENGLASE FAMILY.
                                                                       COFACTOR: MAGNESIUM IS REQUIRED
                                                                                                                                                                                                                                                                                                                                G
                                                          THE DIMER (BY SIMILARITY).
                                                                                   H(2)0.
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ER 1 1
AF258670; AAF72641.1; -.
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13; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38299 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                             72.2%;
81.2%;
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81.2%;
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Last annotation update)
NON-NEURON (FRAGMENT).
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 11;
Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Veri
Sciurognathi;
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                        (BY SIMILARITY)
                                                                       CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae;
                                                                                               databases.
= PHOSPHOENOLPYRUVATE +
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                                                                       AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                        Collembola;
                                                                                                                                                                                                                                             (2-PHOSPHO-D-
                                                                       STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                  0
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RESULT
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ID Q9
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Best Local S
Matches 13
                                                                                                                                                                                                                       Matches
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Best Local
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Pfam; PF00113; enclase; 1.
PRINTS; PR00148; ENCLASE.
ProDom; PD000902; Enclase; 1.
PROSITE; PS00164; ENCLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- CÓFÁCTOR: MAGNESIUM IS REQUIRED FO)
THE DIMER (BY SIMILARITY).
-1- PATHMAY: GLYCOLYSIS:
-1- SUBUNIT: HOMODIMER (BY SIMILARITY)
-1- SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=20063780; PubMed=10594174;

Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;

"Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes.";

J. Mol. Evol. 49:729-735(1999).

-I- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
Q9PTX5
                                                                                                                                                                                                                                                                                                                                         Glycolysis; Lyase; Magnesium.
NON_TER 1 1
SEQUENCE 394 AA; 42583 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO THE ENOLASE EMBL; AB025329; BAA88482.1; -. HSSP; P56252; 1PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lampetra reissneri.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Petromyzontiformes; Petromyzontidae; Lampetra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9PTX6;
01-MAY-2000
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ProDom; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENOLASE-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7753;
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                                                                                                                       345
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                                                                                                                                                1 LVVGLCTCQIKTGPAC 16
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                                                                                                                       LVVGLCTGQIKTGAPC
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                                                                                                                                                                                                                  l Similarity 81.:
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
13; Conserv
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                         42583 MW;
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                                                                                                                                                                                                                  Score 65; DB
Pred. No. 0.00
0; Mismatches
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PRT;
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                                                                                                                                                                                                                                                                                                                                         BC585FE6C712A3D2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394
395
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                                                                                                                                                                                                                                      DB 13;
0.0013;
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0.0013;
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                                                                                                                                                                                                                                                                Length 394;
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                                                                                                                                                                                                                  0;
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9PTX5;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC. 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
                                                                                                                                                                                                                                   Q9U5F7 PRELIMINARY; PRT; 395 AA.
Q9U5F7;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
ELYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - I- PATHWAY: GLYCOLYSIS.
- I- SUBUNIT: HOMODIMER (BY SIMILARITY).
- I- SUBCELLULAR LOCATION: CYTOPLASMIC (IO: SIMILARITY: TO THE ENOLASE FAMILY.
EMBL; AB025330; BAA88483.1; -.
HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-20063780; PubMed=10594174;

MEDLINE-20063780; PubMed=10594174;

Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;

"Monophyly of lampreys and hagfishes supported by nucl
genes.";
                                                 genes.";
J. Mol. Evol. 49:729-735
-i- CATALYTIC ACTIVITY:
                                                                                                                   TISSUE=LIVER;
MEDLINE=20063780; PubMed=10594174;
                                                                                                                                                                                           Eptatretus burgeri (Inshore hagfish).
Eukaryota; Metazoa; Chordata; Craniata;
Myxinidae; Eptatretinae; Eptatretus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycolysis; Lyase; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00148; ENOLASE.
PRODOM; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
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-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Petromyzontiformes; NCBI_TaxID=7753;
        H(2)0.
-i- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS
THE DIMER (BY SIMILARITY).
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00113; enolase;
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                                                                                                                                                                             Myxinidae; Eptatretinae; Eptatretus.
NCBI_TaxID=7764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENOLASE-2
                                                                                            Kuraku S., Hoshiyama D., Katoh K., Sumonophyly of lampreys and hagfishes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000941; Enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lampetra reissneri.
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                                                                  49:729-735(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA; 43266 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FRAGMENT).
                                                 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 13;
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8591D68662DA8544 CRC64;
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                                                                                                           Suga
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                                                                                            H., Miyata T.;
pported by nucl
                                                                                                                                                                                                           Hyperotreti;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 395;
                          AND FOR STABILIZING
                                                                                             nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                             DNA-coded
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PATHWAY:

GLYCOLYSIS

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Best Local S
Matches 13
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Best Local Similarity
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
-01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
Penaeus monodon (Penoeid shrimp).
Eumalacostraca; Eucarida; Decapoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096656;
                                                                                                                       METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         **Boonchouy C., Boonyawan B., Panyim S., Sonthayanon B.;

"Complete cDNA sequence of phosphopyruvate hydratase (enclase) from marine shrimp, Penaeus monodon.";

Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                 Glycolysis;
ACT_SITE
                                                                                                                                                                                                                                                              H(2)O.

-!- COFACTOR: MAGNESIUM IS REQUIRED FOR THE DIMER (BY SIMILARITY).

-!- PATHWAY: GLYCOLYSIS.

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (
-!- SUBCELLULAR TO THE ENOLASE FAMILY.
                                                                                                                                                                        PRINTS; PR00148; ENOLASE.
PRODOM; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                              Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                          EMBL; AF100985; AAC78141.1; -. HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=ABDOMINAL MUSCLES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycolysis; Lyase; Magnesium.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB025326; BAA88479.1; HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penaeidae; Penaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000902; Enolase; 1. PROSITE; PS00164; ENOLASE; 1.
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386
                                                                                                                                                                                                                               InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LVVGLCTCQIKTGPAC 16
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     LVVGLCTGQIKTGAPC
                               LVVGLCTCQIKTGPAC 16
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                                                         l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00148; ENOLASE.
                                                                                                                      Lyase; Magnesium; Pyruvate.
343 343 BY SIMILARITY.
355 355 MAGNESIUM (BY SIMII
434 AA; 47265 MW; EB575C6FB541ABD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 AA;
                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43131 MW;
                                                                    72.2%;
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      401
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                                                       Score 65; DB Pred. No. 0.00
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D351C6700DDC75CD CRC64;
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                                                                                                                                                                                                                                                                                                                                    FOR CATALYSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434
                                                                    DB 5;
0.0014;
                                                                                                                                                                                                                                                                                (BY SIMILARITY)
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0.0013;
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                                                                                                                      SIMILARITY)
1ABD3 CRC64;
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                                                                                Length 434;
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                                                       Indels
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Best Local Similarity
Matches 13; Conser
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             Mannen H., Li S.S.-L.;

"Molecular evidence for a clade of turtles.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ

EMBL; AF072588; AAD41645.1; -.

HSSP; P56252; 1PDZ.
                                                                                                                         Trachemys scripta elegans.
Trachemys scripta elegans.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Tostndines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
GLYCERATE HYDRO-LYASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycolysis; Lyase; Magnesium.
ACT_SITE 341 341
METAL 353 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular evidence for a clade of turtles.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                        Testudines; Cryptodira; NCBI_TaxID=31138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00148; ENOLASE.
ProDom; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000941; Enolase.
Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sceloporus undulatus (Eastern fence lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF072587; AAD41644.1; -. HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: GLYCOLYSIS.

!- SUBUNLT: HOMODIMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (

-!- SIMILARITY: TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \mbox{\ensuremath{H(2)0}}. -!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
                                                                                 TISSUE=MUSCLE;
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mannen H., Li S.S.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
                                                                                                                                                                                                                                                                                                                          384 LVVGLCTGQIKTGAPC
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IPR000941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            341 BY SIMILARITY.
353 MAGNESIUM (BY SIMILARITY)
47493 MW; 6E377E0F0A767E11 CRC64;
Enclase
                                                                                                                                                                                                                                                                                                                                                                                           72.2%;
81.2%;
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                                                                                                                                                                                             Last sequence up
Last annotation
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RESULT
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                                                                                                                                                    Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                   -!- PATHWAY: GLYCOLYSIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY
-!- SIMILARITY: TO THE ENOLASE FAMILY.
EMBL; AF072589; AD441646.1; -.
HSSP; P56252; 1PDZ.
InterPro; IPR000941; Enolase.
Pfam; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
 Q9PVK2;
Q9PVK2;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9W7L0;
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                     Glycolysis; Lyase; Magnesium.
ACT_SITE 341 341
METAL 353 353
                                                                                                                                                                                                                                                                                                                                                                                                                    Mannen H., Li S.S.-L.;
"Molecular evidence for a clade of turtles.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                       PRINTS; PRO0148; ENOLASE.
ProDom; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00113; enolase; 1. PRINTS; PR00148; ENOLASE. ProDom; PD000902; Enolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Booidea; Pythonidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=51751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Python regius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                        384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384
                                                                                                                                                               Local Similarity
                                                                                                                             1 LVVGLCTCQIKTGPAC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LVVGLCTCQIKTGPAC
                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                             H(2)0.
                                                                                                       LVVGLCTGQIKTGAPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVVGLCTGQIKTGAPC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
13; Conser
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                                                                                                                                                                                                             353
434 AA;
             (TrEMBLrel. (TrEMBLrel.
  (TrEMBLrel.
                                                                                                                                                    Conservative
                                               PRELIMINARY;
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                                                                                                                                                             72.2%;
81.2%;
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 13,
13,
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Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                    BY SIMILARITY.
MAGNESIUM (BY SIMILARITY).
F242F93E6D467033 CRC64;
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                                                                                                                                                             Score 65; I
Pred. No. 0.
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                                               PRT;
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                                                                                                                                                 Mismatches
                                               434
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                                               A
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                                                                                                                                                                        Length 434;
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RESULT
Q9NG71
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O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
GLYCERATE HYDRO-LYASE) (FRAGMENT).
                     -!- PATHWAY: GLYCOLYSIS.
-!- SUBGUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELULAR LOCATION: CYTOPLASMIC (
-!- SIMILARITY: TO THE ENOLASE FAMILY.
EMBL; AF258666; AAF72637.2;
-Interpro; IPR000941; Enolase.
Pfam; PF00113; enolase; 1
                                                                                                                                                  STRAIN=LPO156_406;
Regier J.C., Shultz J.W.;
"Enclase as a phylogenetic marker.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Limulus polyphemus (Atlantic horseshoe crab)
Eukaryota; Metazoa; Arthropoda; Chelicerata;
Limuldae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
Alligator mississippiensis (American alligator).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria, Crocodylidae; Alligatorinae; Alligator.
                                                                                                             -!- COFACTOR: MAGNESIUM IS REQUIRED THE DIMER (BY SIMILARITY).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Q9NG71
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-!- SIMILARITY: TO THE ENGLASE EMBL; AF072586; AAD41643.1; -- HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mannen H., Li S.S.-L.;
"Molecular evidence for a clade of turtles.";
Mol. Phylogenet. Evol. 13:144-148(1999).
             PRINTS;
                                                                                                                                                                                                                                             NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000902; Enolase; 1. PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99439677; PubMed=10508547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8496;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                          384 LVVGLCTGQIKTGAPC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycolysis; Lyase; Magnesium.
EQUENCE 434 AA; 47322 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LVVGLCTCQIKTGPAC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conserv
PR00148; ENOLASE. PD000902; Enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00148; ENOLASE.
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                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
Enolase;
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81.2%;
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                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                            FOR
                                                                                                                                                                                                                                                                                                                                                                           251
                                                                         (BY SIMILARITY)
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                                                                                                                           CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                                                                                                                                    Merostomata; Xiphosura;
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= PHOSPHO
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                                                                                                                                                   PHOSPHOENOLPYRUVATE
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                                                                                                                           STABILIZING
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RESULT 15
Q9NG73
ID Q9NG73
AC Q9NG73
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 01-EMPORE
OC EMMESO
OC EMMESO
OC CAMPOR
OX NCBL_T
RN [1]
RP SEQUEN
RC STRAIN
RA REGIET
RT "Enola
RL SUBMit
CC -!- SI
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Search completed: May 8,
Job time: 112 sec
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0148; ENOLASE.
PRODOM; PD000902; ENOLASE; 1.
PROSITE; PS00164; ENOLASE; 1.
Glycolysis; Lyase; Magnesium.
NON_TER 1 1 1
NON_TER 159 159
SEQUENCE 159 AA; 17547 MW;
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Q1-QCT-2000 (TremBLrel. 15, Created)
Q1-QCT-2000 (TremBLrel. 15, Last sequence update)
Q1-QCT-2000 (TremBLrel. 17, Last annotation update)
Q1-JUN-2001 (TremBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
Eumesocampa frigilis.
Eumesocampa frigilis.
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NON_TER
SEQUENCE
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H(2)0.

ICOPACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).

I PATHWAY: GLYCOLYSIS.

I SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

INTERPROPERTY: TO THE ENOLASE FAMILY.

EMBL; AP258664; AAF72635.1; -.

Interpro; IPR000941; Enolase.

Pfam; PF00113; enolase; 1.
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NCBI_TaxID=109745;
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                                                                                                                                 138 LVVGLSTGQIKTGAPC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 LVVGLCTGQIKTG 242
                                                                                                                                                              1 LVVGLCTCQIKTGPAC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LVVGLCTCQIKTG 13
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251 AA;
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17547 MW;
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27452 MW;
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92.38;
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75.0%;
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                                                                                                                                                                                                                                  Score 55; DB 5; Pred. No. 0.037; O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   448E41A6DF6664D0 CRC64;
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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        Match
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      BLOSUM62
Gapop 10.0 , Gapext 0.5
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90
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8, 2002, 11:44:44 ; Search time 10.17 Seconds (without alignments) 57.683 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length DB
      ENOB_CHICK
ENOB_MOUSE
ENOB_RABIT
ENOB_RAT
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ENOG_HUMAN
ENOG_MOUSE
ENOC_CHOKA
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ENOA_CHICK
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                                                                                                                                                                                                                                                                       P21550 mus musculu
P25704 oryctolar
  Q05524
Q9xsj4
P42897
P19140
P51913
P06733
P17182
                                                                                                                                                                                                                                                                                                     P04764
P07322
P13929
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                      2 homarus gam
4 xenopus lae
4 loligo peal
6 schistosoma
7 schistosoma
7 gallus gall
7 caenorhabdi
7 drosophila
7 fasciola he
s arabidopsis
lycopersico
zea mays (m
l alnus gluti
hevea brasi
hevea brasi
                                                                               cunninghame
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rattus norv
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gallus gall
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homo sapien
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| 45 | 44 | 43 | 42 | 41 | 40 | ω 9 | 38 | 37 | 36 | 35 5 | 34 |
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| 46 | 46 | 46 | 46.5 | 46.5 | 47 | 47 | 48 | 49 | 49 | 49 | 50 |
| 51.1 | 51.1 | 51.1 | 51.7 | 51.7 | 52.2 | 52.2 | 53.3 | 54.4 | 54.4 | 54.4 | 55.6 |
| 137 | 137 | 126 | 436 | 436 | 446 | 436 | 372 | 446 | 444 | 436 | 445 |
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| THN6_HORVU | THN3_HORVU | THN1_WHEAT | ENO2_YEAST | ENO1_YEAST | ENO_PLAFA | ENO1_ENTHI | ENO_CHLRE | ENO1_MAIZE | ENO_MESCR | ENO_NEOFR | ENO_RICCO |
| P09618 hordeum vul | | | | | | | | P26301 zea mays (m | | P42894 neocallimas | P42896 ricinus com |

ALIGNMENTS

Query Match

ENO2_HEVBR

82.2%; Score 74; DB 1; Length 458;

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RESULT 2
ENOA_BOVIN
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                                  δÃ
                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
-1- PARHMAY: GLYCOLYSIS.
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
                                                                                                                                                                                Lyase; Gl
INIT_MET
ACT_SITE
                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Co
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENOA_BOVIN
                                                                                                                                                                                                                     Pfam; PF00113; enolase; 1 PRINTS; PR00148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XSJ4;
                                                                                                                             SEQUENCE
                                                                                                                                            METAL
                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                       EMBL; AF149256; AAD33073.1; -.
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                                                                                                                                                                                                                                               [nterPro;
          383 LVVGLCTGQIKNGPPC
                                    1 LVVGLCTCQIKTGPAC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVVGLCTCQIKTGPAC
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                                                             l Similarity
13; Conser
                                                                                                                                                                                                       Glycolysis; Magnesium; Multigene family.
                                                                                                                                                                                                                                              IPR000941; Enolase.
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157
244
292
317
433
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                                                                                                                             AA;
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244
292
317
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                                                                                                                              47145 MW;
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Pred. No.
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                                                                                                                             B004E965C46F2E0C CRC64;
                                                              Mismatches
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(BY SIMILARITY).
(BY SIMILARITY).
                                                                                        DB 1;
                                                                          0015;
                                                                                     Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHOENOLPYRUVATE
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                                                              Indels
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RESULT ENO_ALLMI
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RESULT 4
ENOA_ANAPL
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SEQUENCE
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P42897;
01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
                                               p19140;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (TAU-CRYSTALLIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPROUUY41; ENULANCE; 1.
Pfam; PF00113; enolase; 1.
ProDom; PD000902; ENOLASE; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular evidence for the origin of birds."; Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENO_ALLMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L28078; AAA53671.1; -. HSSP; P56252; 1PDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=94195794; PubMed=8146164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  ENOA_ANAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyase; Glycolysis; Magnesium.
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PACHWAY: GLYCOLYSIS.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SUBUNIT: HOMODIMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE DIMER (BY SIMILARITY).
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223
271
296
395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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                                                                                                                                                                                                                     STANDARD;
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223
271
296
395
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81.2%;
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Pred. No. 0.004;
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Eukaryota; Anas platyrhynchos

Metazoa;

(Domestic

duck)

Chordata;

Craniata; Vertebrata;

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RESULT 5
ENOA_CHICK
ID ENOA_C
AC P51913
DT 01-OCT
DT 01-OCT
DT 15-JUL
DE ALPHA
DE (PHOSP
OS Gallus
OC EUKATY
OC Archos
OC Gallus
OC MCBL_T
RN [1]
RP SEQUEN
RC STRAIN
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                     P51913;
D1-OCT-1996 (Rel. 34, Created)
D1-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE (PHOSPHOPYRUVATE HYDRATASE).
STRAIN=WHITE LEGHORN; TISSUE=Kidney;
                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INIT_MET
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                                                                                                                                                                                      Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00148; ENOLASE.
PRODOM; PD000902; Enolase;
PROSITE; PS00164; ENOLASE;
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EMBL; X14195; CAA32409.1; -.
PIR; A32132; A32132
HSSP; P56252; 1PDY.
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J. Cell Biol. 107:2729-2736(1988).
-!- FUNCTION: BOTH AN ENZYME AND A LENS STRUCTUR
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE =
                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENOA_CHICK
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00113; enolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wistow G.J., Lietman T., Williams L.A., Horwitz J., Piatigorsky J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wistow G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89079778; PubMed=2462567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryonic lens;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LVVGLCTCQIKTGPAC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: GLYCOLYSIS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVVGLCTGQIKTGAPC
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0 0 0
0 11TE 157 157 187
244 244 MA
242 292 MA
317 317 MA
NCE 433 AA; 47108 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Eute
Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.2%;
81.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eye lens protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGNESIUM (BY SIMILARITY).
AGNESIUM (BY SIMILARITY).
AGNESIUM (BY SIMILARITY).
1AED78B08A66E84D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433
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0.0043;
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                                                                                                                                                                                                                 Euteleostomi;
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                                                                                                                                                                                      Phasianinae;
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                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                 ENOA_HUMAN STANDARD; PRT; 433 AA.
P06733; Q16704; Q9UM55;
01-JAN-1988 (Rel. 06, Created)
01-APR-1988 (Rel. 07, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
SEQUENCE
                                                                            Giallongo A., Feo S., Moore R., Croce C.M., Molecular cloning and nucleotide sequence
                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                      SEQUENCE FROM N.A.
                                                     Proc. Natl.
                                                                                                        SEQUENCE FROM N.A. MEDLINE=86313654; PubMed=3529090;
                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: GLYCOLYSIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biochem. 117:554-559(1995).
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE =
           MEDLINE=90323004;
                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                        NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyase; Glycolysis; Magnesium;
INIT_MET 0 0
ACT_SITE 157 157 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tanaka M., Maeda K., Nakashima K.; "Chicken alpha-enclase but not beta-enclase has tyrosine-phosphorylation site: cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00148; ENOLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P56252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- COFACTOR: MAGNESIUM IS REQUIRED FOR THE DIMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95355305; PubMed=7629021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                     383 LVVGLCTGQIKTGAPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               1 LVVGLCTCQIKTGPAC 16
                                                                                                                                                                                                             OR ENO1L1
                                                                 alpha enolase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00113; enolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                     Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                    Sci.
        PubMed=2373081;
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81.2%;
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                                                  U.S.A. 83:6741-6745(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 1;
Pred. No. 0.0043;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).
                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93AD6B0A7AD99910
                                                                                            Croce C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYSIS
                                                                            , Showe L.C.;
of a full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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Giallongo A., Oliva D.,

Cali L.,

Barba G.,

Barbieri G.,

Feo : :

MAGNESIUM

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TARAS A REPARA A PER PARA BARA BARAS SOS SOS SOS SOS SOS DA SAR BARAS A REPARA BARAS BARAS
                                                                                                                                                                                                                                                                                                                                                    EMBL; M14328; AAA52387.1; -
EMBL; X16288; CAA34360.1; J
EMBL; X16289; CAA34360.1; J
EMBL; X16290; CAA34360.1; J
EMBL; X84907; CAA59331.1; -
EMBL; W84907; CAA59335.1; -
EMBL; W8968; AAC39355.1; -
PIR; A29170; A29170.
PIR; S11696; S11696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97295306; PubMed-9150948;
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burge
"A two-dimensional gel database of human colon c
Electrophoresis 18:605-613(1997).
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96422099; PubMed=8824716; Walter M., Leidenberger F.A., Schweppe K.W., Berg H., Northemann W.; "Autoreactive epitopes within the human alpha-enolase and their recognition by sera from patients with endometriosis."; J. Autoimmun. 8:937-945(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mohamad R.M., Hamdan M.Y., Maki A., & "Induced expression of alpha-enolase cell lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 269-280 AND 306-320.
MEDLINE-95307697; PubMed-7787969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onyango P., Lubyova B., Gardellin Molecular cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Colon carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzyme Protein 48:37-44(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 50:187-198(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98317532; PubMed=9653645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 165-433 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Endometrium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of the human gene for alpha-enolase."; Eur. J. Biochem. 190:567-573(1990).
                                                                                                                          PROSITE;
                                                                                                                                                                                                      Pfam; PF00113; enolase;
                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                             Aarhus/Ghent-2DPAGE;
                                                                                                                                                                                                                                                                                                           Aarhus/Ghent-2DPAGE;
                                                                                                                                                                                                                                                                                                                                   HSSP; P56252; 1PDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: GLYCOLYSIS SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOST TISSUES, BETA IS LOCALIZED IN FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                                                                                                                                                          172430;
;; Glycolysis; Magnesium; M
MET 157 157 BY
TTE 157 244 244 MAC
                                                                                                                    PD000902; Enclase; PS00164; ENCLASE;
                                                                                                                                                                                                                            IPR000941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOLYSIS.
                                                                                                                                                                              ENOLASE.
                                                                                                                                                                                                                                                                                1325;
5406;
                                                                                                                                                                                                                            Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maki A., Al-Katib A.;
ha-enolase in differentiated
                                                                                                                                                                                                                                                                                  NEPHGE.
                   BY SIMILAR MAGNESIUM
                                                                                            Multigene family.
                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P., Kurzbauer R., analysis of five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUSCLE
                   (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burgess A.W., olon carcinoma
                     SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α.,
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ENOA_MOUSE
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                                                                                                                                                                                                                                                   RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Matsuda H.A., Ashburner M., Bano H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Slake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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CONFLICT
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P17182; Q9DCY7;

01-AUG-1990 (Rel. 15, Created)

20-AUG-2001 (Rel. 40, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUV
                                                                                                                                                                                                                                                 Wynshaw-Boris A., Yoshida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
                                                                                                                                                -!- COFACTOR: MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequences of cDNAs alpha and mouse brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic
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                                  SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT I
                                                                                         PATHWAY: GLYCOLYSIS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR ENO-1
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Rodentia;
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81.2%;
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                                                                                                                                                \mathbf{SI}
                                                                                                                                                                                    2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
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LOCALIZED IN MUSCLE TISSUE.
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F -> S (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Murinae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGNESIUM (BY SIMILARITY).
AGNESIUM (BY SIMILARITY).
-> S (IN REF. 3).
B2028684C33140B5 CRC64;
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                                                                                                                                                  FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 1;
. 0.0043;
                                                                                                                                                  CATALYSIS
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Fukuda S.,
manaka I.,
Saito R.,
                                                                                                                                                  STABILIZING
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MOST TISSUES, FOUND ONLY IN

BETA IS

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AND GAMMA

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RESULT
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                                                                                                                                                                                                                                                                                               ENGA_RAT STANDARD; PRT; 433 AA.
PQ4764;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1988 (Rel. 36, Last annotation update)
ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE).
                                                                                                                                                     MEDLINE=85242108; PubMed=2989793; Sakimura K., Kushiya E., Obinata M., Takahashi Y., Sakimura roloning and the nucleotide sequence of cDNA to mi non-neuronal enolase (alpha alpha enolase) of rat brain and nucleic Acids Res. 13:4365-4378(1985).
                                                                                                                                                                                                                                                                                                                                                                                                           RAT
                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                      Submitted (JAN-1986)
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INIT_MET
ACT_SITE
                                                                                                                   Takahashi Y
                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P56252; 1PDY.
SWISS-2DPAGE; P17182; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X52379; CAA36605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LVVGLCTCQIKTGPAC 16
PATHWAY: GLYCOLYSIS.
SUBUNIT: HOWODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC
TISSUE SPECIFICITY: THREE CLASSES
                                                                                       CATALYTIC ACTIVITY:
                                                                COFACTOR: MAGNESIUM
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                                                      THE DIMER.
                                                                             + H(2)0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycolysis; Magnesium; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD000902; Enolase; 1. PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR00148; ENOLASE.
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244
292
317
358
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81.2%;
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                                                                                       the EMBL/GenBank/DDBJ
2-PHOSPHO-D-GLYCERATE
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                                                              REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No.
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
L -> P (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                              FOR CATALYSIS
OF ENOLASE ISOENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.0043;
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                                                                                   databases.
= PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 433;
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HAVE BEEN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-Muscle;
MEDLINE-95355305; PubMed=7629021;
Tanaka M., Maeda K., Nakashima K.;
Tchicken alpha-enclase but not beta-enclase has a Src-dependent
"Chicken alpha-enclase but not beta-enclase has a src-dependent
                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1988 (Rel. 07, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLY
(PHOSPHOPYRUVATE HYDRATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P07322;
01-APR-1988 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                         enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                          Biochem.
                                                                                                    MEDLINE=87075592; PubMed=3539098; Russell G.A., Dunbar B., Fothergill Gilmore L.A.;
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X02610; CAA26456.1; -. PIR; A23126; A23126. HSSP; P56252; 1PDY.
                                                                                         Russell G.A., Dunbar B., Fothergil
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENOB_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE

      Lyase; Glycolysis; Magnesium; Multigene family.

      INIT_MET
      0

      0
      0

      ACT_SITE
      157
      157

      METAL
      244
      MAGNESIUM (BY SIMI METAL

      METAL
      292
      MAGNESIUM (BY SIMI MAGNESIUM (BY SIMI METAL

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00148; ENOLASE.
ProDom; PD000902; Enolase;
PROSITE; PS00164; ENOLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00113; enolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000941; Enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 LVVGLCTGQIKTGAPC
                                                                                                                                                                       Biochem. 117:554-559(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LVVGLCTCQIKTGPAC 16
          COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                         CATALYTIC ACTIVITY:
                              + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                 J. 236:115-126(1986).
LYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398
                                                                                                                                                                                                                                                                                                                                                                                                            annotation update)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGNESIUM (BY SIMILA
MAGNESIUM (BY SIMILA
MAGNESIUM (BY SIMILA
W; F1A25F010C276E7C (
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                          of:
                                                                                         chicken skeletal-muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433
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Y SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                        P13929;
01-JAN-1990
01-OCT-1993
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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METAL
CONFLICT
MEDLINE-90067857; PubMed=2587223; MEDLINE-90067857; PubMed=2587223; Peshavaria M., Hinks L.J., Day I.N.M.; Peshavaria of human muscle (beta) enclase mRNA and "Structure of human muscle (beta) enclase mRNA and
                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
(SKELETAL MUSCLE ENOLASE) (MSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000902; Enolase; PROSITE; PS00164; ENOLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D37901; BAA07133.1; -. PIR; A23850; A23850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENOB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: GLYCOLYSIS.
                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 LVVGLCTGQIKTGAPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LVVGLCTCQIKTGPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00113; enclase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P56252; 1PDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycolysis; Magnesium; Multigene family; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
48
118
208
208
257
265
265
308
330
342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.2%;
81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLATION.
BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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MAGNESIUM (BY SIMILARITY).
E -> D (IN REF. 2).
P -> L (IN REF. 2).
CK -> SH (IN REF. 2).
G -> D (IN REF. 2).
H -> D (IN REF. 2).
H -> D (IN REF. 2).
HT -> DP (IN REF. 2).
Y -> L (IN REF. 2).
F -> S (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
K -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 1;
Pred. No. 0.0043;
                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9BC2FB5FB910C254 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 433;
                                                 protein
                                                                                                                                                                                                                                                              Euteleostomi;
                                                       deduced
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                                                                                                              SO THE FET TITES OF A PROPERTY OF A PROPERTY
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S15933; S15933.
PIR; S06756; S06756.
PIR; S14759; S14759.
PIR; S31650; S31650.
PIR; S33330; S33330.
                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                     Lyase; G. INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X16504; CAA34513.1; -. EMBL; X51957; CAA36216.1; -. EMBL; X55976; CAA39446.1; -. EMBL; X56833; CAA40163.1; -. EMBL; X56833; CAA40163.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91222137; PubMed=1840492;
Peshavaria M., Day I.N.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. [2]
                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00148; ENOLASE. ProDom; PD000902; Enolase; PROSITE; PS00164; ENOLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 214:367-374(1993).
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-93292497; PubMed=8513787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90245587; PubMed-2336366; Cali L., Feo S., Oliva D., Giallongo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Differential splicing forms of mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Giallongo A.,
                                                                                                                 SEQUENCE
                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF0011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 131370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feo S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of a cDNA encoding the human muscle-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular structure of the human muscle-specific enolase gene
                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural features of the human gene for muscle-specific enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ENO3)."
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SUBGELLULAR LOCATION: CYTOPLASMIC.

SUBSCELLULAR LOCATION: CYTOPLASMIC.

TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS FOUND ONLY IN NERVOUS TISSUE.

FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P56252;
                                                                                                                                                                                                                                                                                                                                                 Glycolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. 275:427-433(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1PDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Res. 18:1893-1893(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venturella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17:8862-8862(1989).
                                                                                                                                                                                                                                                                                                                     Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in
                              72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the 5'-untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S., Oliva D., Barbieri G.,
                                                                                                                 WW.
                                                                                                           BY SIMILARITY.

BY SIMILARITY.

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

V-> A (IN REF. 3).

V-> N (IN REF. 1 AND 2).

K-> N (IN REF. 1 AND 2).
                           Score 65;
                                                                                                                                                                                                                                                                                                                                                       Multigene family.
                              BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                        Length 433
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Matches
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                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental expression.";
Proc. Natl. Acad. Sci. U.S.A. 86:4445-4449(198
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE
                          HSSP;
                                                                                                                                          EMBL;
                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                 the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peterson C.A., Cho M., Rastinejad F., Blau H.M.;
"Beta-enclase is a marker of human myoblast heterogeneity
differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/C; TISSUE=Liver;
Lamande N., Brosset S., Keller A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1991 (Rel. 18, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
(SKELETAL MUSCLE ENOLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Legault-Demare L., Lazar M.;
Murine muscle-specific enolase: cDNA cloning, sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamande N., Mazo A.M., Lucas M., Montarras D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89282789; PubMed=2734297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P21550;
01-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92290133; PubMed=1339335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENO3 OR ENO-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENOB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383
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                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA
FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                            European Bioinformatics Institute. The by non-profit institutions as long filed and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: MAGNESIUM IS
                                           $17109; NOMSB.
A33921; A33921.
$29675; $29675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: GLYCOLYSIS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE DIMER.
                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVVGLCTGQIKTGAPC 398
                                                                                                                X61600; CAA43797.1; -. X62667; CAA44540.1; -. M20745; AAA37554.1; -. X57747; CAA40913.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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P21550; MOUSE
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86:4445-4449(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                  There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
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; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                        restrictions
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the EUropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             directed mutagenesis (E417L) of the gene, expression of the wild-typ and mutant genes in Escherichia coli.";
Thesis (1995), Concordia University, Montreal / Quebec, Canada.
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENOB_RABIT STANDARD; PRT; 433 AA. P25704; Q9NON6; 01-MAY-1992 (Rel. 22, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE (SKELETAL MUSCLE ENOLASE).
                                                                                                                                                                                                                                                                                                                     Then cDNA cloning of rabbit muscle-specific enclase gene, site
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               "The primary structure of rabbit muscle J. Protein Chem. 9:427-432(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                              chin c.c.Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91113295; PubMed=2275753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
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ProDom; PD000902; Enolase; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Muscle;
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Pfam; PF00113; enolase; 1.
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                                                                                                                            PARHWAY: GLYCOLYSIS.

SUBUNIT: HOMODIMER.

SUBCELLULAR LOCATION: CYTOPLASMIC.

SUBCELLULAR LOCATION: CYTOPLASMIC.

SUSSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT I MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA I FOUND ONLY IN NERVOUS TISSUE.
                                                                                                                    SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                    COFACTOR: MAGNESIUM
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                                                                                                                                                                                                                                          THE DIMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cuniculus (Rabbit).
Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
AG -> NA (IN REF. 3).
B318B763382D3FA8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY. MAGNESIUM (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                              enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
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                                                                                                                                               AND GAMMA IS
                                                                                                                                                                                                                                                    FOR STABILIZING
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EMBL outstation

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RESULT :
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Best Local S
Matches 13
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ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
(SKELETAL MUSCLE ENOLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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INIT_MET
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TWASE; Glycolysis;
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PIR; /
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(beta
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-27 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WISTAK;
MEDLINE-89121113; PubMed-2914621;
Witchi H., Takayama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                  "Structure and expression of rat muscle-specific enolase gene.";
FEBS Lett. 277:78-82(1990).
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUV
                                                                                                                                                                                                                                                                                                                                 Sakimura K., Kushiya E.,
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91099531; PubMed=2269373;
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                                                                                                                                                                                                                                                                                                                rakahashi Y.;
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                                  MOST TISSUES, BETA IS LOCALIZED IN MUSCLE FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRES
                                                                                                                                                       PATHWAY: GLYCOLYSIS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                COFACTOR: MAGNESIUM
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A37210; A37210.
; P56252; 1PDY.
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SWISS-PROT
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Lett. 242:425-430(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cloning and nucleotide sequence
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Rodentia;
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81.2%;
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copyright.
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Sciurognathi;
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                                                                            TISSUE,
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through
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P09104;
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"Human gamma enolase: isolation of a normal and tumor tissues of human ori J. Neurosci. Res. 19:450-456(1988).
                                                          van Obberghen E.,
Lazzarini R.A.;
                                                                                              MEDLINE=88259288;
                                                                                                                                       SEQUENCE
                                                                                                                                                                                             enolase.
                                                                                                                                                                                                                                                                            SEQUENCE
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Kamholz PubMed=3385803;

J.,

Bishop

J.G.

III,

Zomzely-Neurath

of human origin.";

CDNA

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"Complete amino acid sequence of the r of enclase (NSE) from human brain and non-neuronal alpha form (NNE)." Eur. J. Biochem. 178:413-417(1988).
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MG-2001 (Rel. 40, Last annotation update)
GAMMA ENOLASE (EC 4.2, 1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y00979; CAA68788.1; -.
EMBL; X57774; CAA40920.1; -.
EMBL; S02072; S02072.
HSSP; P56252; 1PDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                   MEDLINE-90006764; PubMed=2792767;
Oliva D., Barba G., Barbieri G., Giallongo A., I
"Cloning, expression and sequence homologies of
                                                                                                                                                                                                                            MEDLINE=89091176; PubMed=3208766;
                                                                                                                                                                                                                                                TISSUE=Retina;
                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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244 244 M

292 292 M

317 317 M
79:355-360(1989).
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PD000902; Enolase;
PS00164; ENOLASE
                                                                                                                                                                                   S.M., Dunbar B., Fothergill J., Hinks L., Day
e amino acid sequence of the neurone-specific
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ENOLASE;
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AGNESIUM (BY SIMILARITY).
AGNESIUM (BY SIMILARITY).
4C2CBDB12DBA536D CRC64;
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Day I.N.M., Allsopp M.T.E.P., Moore D.C.M., Thompson F
"Sequence conservation in the 3'-untranslated regions specific enolase, lymphokine and protooncogene mRNAs."
FEBS Lett. 222:139-143(1987).
                                                                                                                                                          Pfam; PF00113; enolase; 1. PRINTS; PR00148; ENOLASE. PRODOm; PD000902; Enolase; 1. PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Hematopoietic;
MEDLINE=91257823; PubMed=2045099;
Oliva D., Cali L., Feo S., Giallongo A.;
                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96303695;
                                                                           VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: GLYCOLYSIS.
SUBUNIT: HOMODIMER.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT I MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA I FOUND ONLY IN NERVOUS TISSUE.
FOUND ONLY IN NERVOUS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                 L; X13120; CAA31512.1; -.
L; M22349; AAB59554.1; -.
L; M36768; AAA52388.1; ALT_INIT.
L; X51956; CAA36215.1; -.
L; X47924; AAB51320.1; -.
L; X14327; CAA32505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: MAGNESIUM
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                                                                                                                                                                                                                                             JU0060; NOHUG.
S02077; S02077.
S02616; S02616.
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                                                                                                                                                Glycolysis;
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Q -> E (IN REF. 2, 4
AK -> GC (IN REF. 3)
E -> N (IN REF. 3).
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P -> A.
                                                 /FTId=VAR_002354
T -> A
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RESULT 15
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P17183;

01-AUG-1990 (Rel. 15, Created)

01-AUG-1990 (Rel. 15, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

GAMMA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                  InterPro; IPR000941; Enclase, pfam; PF00113; enclase; 1. PRINTS; PR00148; ENCLASE.
                                                                                                      EMBL; X52380;
                                                                                                                          modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                           the
                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1997) to -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                          Gibbs R.A.;
                                                                                                                                                                                                                                                                                                                                                                                   Ansari-Lari M.A., Oe
Lu J., Gorrell J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequences of cDNAs alpha and mouse brain.";
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PROSITE;
            ProDom; PD000902;
                                                       MGD; MGI:95394; Eno2.
                                                                     HSSP;
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                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                     FOUND ONLY IN NERVOUS TISSUE.
SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                ; AC002397; AAC36002.1; -. $10247; $10247.
                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
                                                                                                                                                                                                                                                                                                     PATHWAY: GLYCOLYSIS.
                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER.
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                                                                                                                                                                                                                                            IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE,
                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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13; Conser
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H., Chinault A.C., Belmo
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ENOLASE;
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47154 MW;
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Rodentia;
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2-PHOSPHO-D-GLYCERATE
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Sciurognathi; Muridae;
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Miller W.,
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KW Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT_MET 0 0 0
FT ACT_SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 433 AA; 47165 MW; B7281132E637D43E CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LVVGLCTCQIKTGPAC 16
Db 383 LVVGLCTGQIKTGAPC 398

Search completed: May 8, 2002, 11:46:32

Job time: 108 sec
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Title:
Perfect score:
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Maximum DB seq length: 2000000000
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| RESULT 2 150026 phosphopyruvate hy N;Alternate names: C;Species: Alligat; C;Date: 21-Feb-199 C;Accession.—F6072 R-Hedges; S.B. Proc. Natl. Acad. A;Title: Molecular A;Reference number A;Reference number A;Reference number A;Reference: 1395: m A;Rocession: 15002 A;Status: prelimin A;Rocession: 15002 A;Status: prelimin A;Rocession: 15002 C;Keywords: 1395: m | Query Matc Best Local Matches 1 LV Qy 1 LV Db 285 LV | RESULT 1 A39579 c-myc promoter-bin C;Species: Homo sa C;Date: 07-Feb-199 C;Accession: A3957 K;Ray, R; Miller, Mol. Cell. Biol. 1 A;Title:-Cloning a A;Reference number A;Reference number A;Reference: 1-335 A;Cross-references A;Map position: 89 C;Keywords: DNA bi | 230 331 332 333 333 333 333 333 333 333 333 |
| pyruvate hy nate names: es: Alligat es: Alligat 21-Feb-199 s, S.B. atl. Acad Molecular ence number sion: I5002 s: prelimin ule type: m ule type: | tch al Simi 7; LVVGLCT LVVGLCT | | ហាហាហាហាហាហាហាហាហាហាហាហាហាហាហា |
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| | 96 O 95 80 | iin M ie re erize MUID MUID 1 | 0000100000000110 |
| .11) alpha - American is (American alligator ion 21-Feb-1997 #text_ 621-2624, 1994 | Score 7; DB 2; Leng; Pred. No. 2.6; 0; Mismatches 0; | BP-1 - human wigion 07-Feb-1992 #tex 1991 1991 atton of a human c-myc :91172204 ID:g180662; PIDN:AAA356 | T45346 JC4508 FEPRR FEPRR T40428 T440428 S45612 C24775 C24775 C24775 C84859 B75550 T088489 B75557 T09244 D8411GNMENTS |
| alligator (fragment) r) _change 22-Jun-1999 translation not shown; to | th 335; Indels 0; Gaps 0; | t_change 22-Jun-1999 promoter-binding protein. 98.1; PID:g180663 | hypothetical prote flagellar biosynth ferredoxin [2re-2s 60s ribosomal protein ferredoxin [re-2s 7-cell receptor ga cytochrome o ubiqu hypothetical prote habd dehydrogenase nabh dehydrogenase plantacyanin precu hypothetical prote |

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C; Superfamily: enolase C; Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase F;1/Modified sits: acetylated amino end (Ala) #status experimental
                                                                                                                                                        A; Molecule type: protein A; Residues: 1-433 <CHI>
                                                                                                                                                                                                                                                                                      R; Chin,
                                                                                                                                                                                                                                                                                                                          phosphopyruvate hydratase (BC 4.2.1.11) beta - rabbit
N;Alternate names: enclase beta
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Dec-1991 #sequence revision 30-Dec-1991 #text_change 05-Aug-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;17/Modified site: acetylated amino end (Ser) #status experimental F;39/Binding site: magnesium 2 (Ser) #status predicted F;209/Active site: Glu #status predicted F;209/Active site: Glu #status predicted F;244,292,317/Binding site: magnesium 1 (Asp, Glu, Asp) #status pr
                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                             A; Reference number: A37210; MUID:91113295
A; Accession: A37210
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A; Residues: 1-9 <GIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Gibson, B.W.; Daley, D.J.; Williams, D. Anal. Biochem. 169, 217-226, 1988
A;Title: Structural elucidation of N-term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Russell, G.A.; Dunbar, B.; Fothergill-Gilmore, Biochem. J. 236, 115-126, 1986
A;Title: The complete amino acid sequence of chi-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphopyruvate hydratase (EC 4.2.1.11), skeletal muscle -
N;Alternate names: enclase, skeletal muscle
C;Species: Gallus gallus (chicken)
C;Date: 22-Jul-1987 #seguence_revision 22-Jul-1987 #text_ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A23850
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     Matches
                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                            Accession: A37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keywords: acetylated amino end; carbon-oxygen lyase; gluconeogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comment: Several tissue-specific enolase isoenzymes are found in vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                     Protein Chem. 9, 427-432, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 LVVGLCT 389
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les 7; Conserv
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                 43.8%; Score 7; 100.0%; Pred. No.
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100.0%; Pred. No. 3.
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.8%;
100.0%;
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Pred. No.
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   Mismatches
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                     DB 2;
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   0;
                                     Length 433;
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A; Introns: 29/1; 61/
C; Complex: homodimer
C; Function:
                                           A;Cross-references: GDB:119872; OMIM:131360
A;Map position: 12p13-12p13
A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2
                                                                                                                                                           C;Comment: Enolase occurs with at least C;Comment: Thr-191 may be important for C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:Y00691; GB:MZ/019
R;Harrington, C.R.; Quinn, G.B.; Hurt, J.;
Biochim. Biophys. Acta 1158, 120-128, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S02077
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 2-3, (0',5-239,'M',241-434 <MCA>
A;Cross-references: EMBL:X13120; NID:g31145; PIDN:CAA31512.1; PID:g930063
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: 264-Ala and 395-Ala were also found
A;Note: 264-Ala and 395-Ala were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Jun-1999
C:Accession: JU0060; S16163; S02077; I56569; S02616; S38303
R;Oliva, D.; Barba, G.; Barbieri, G.; Giallongo, A.; Feo, S.
Gene 79, 355-360, 1989
A;Title: Cloning, expression and sequence homologies of cDNA for human gamma A;Reference number: JU0060; MUID:90006764
A;Accession: JU0060
                                                                                                                                 A; Gene: GDB: ENO2
                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 156-173 <HAR>
                                                                                                                                                                                                                                                                                                      A; Reference number: S38303; MUID: 94002176
A; Accession: S38303
                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Characterisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Besidues: 425-434 < DAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Neurosci. Res. 19, 450-456, 1988
A:Title: Heman gamma enclase; isolation of a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references. GR:X51956; NID:g31164; PIDN:CAA36215.1; PID:g31165
R;McAleese, S.M.; Dunbar, B.; Fothergill, J.B.; Hinks, L.J.; Day, I.N.;
Eur. J. Biochem. 178, 413-417, 1988
A:Title: Complete amino-acid sequence of the neurone-specific gamma iso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: I56569; MUID:88259288
A;Accession: I56569
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Genomics 10, 157-165, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S02616
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A; Residues: 'GC', 29-126,'N', 128-434 <VAN>
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A; Residues: 1-434 <OL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I.N.M.; Allsopp, M.T.E.P.
ett. 222, 139-143, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID:g182117; PIDN:AAA52388.1; Moore, D.C.M.; Thompson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishop, J.G.
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to chloride ions
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
C;Accession: S17109; S18036; S29675; A33921
R;Lamande, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.
submitted to the EMBL Data Library, September 1991
A;Reference number: S17109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phose A;Pathway: gluconeogenesis; glycolysis C;Superfamily: enclase C;Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis: F;2-434/Product: phosphopyruvate hydratase gamma *status predicted <MAT> F;2/Modified site: blocked amino end (Ser) in mature form) (probably acetylated) *status predicted F;40/Binding site: magnesium 2 (Ser) *status predicted F;210,343/Active site: Glu, Lys *status predicted F;210,343/Active site: magnesium 1 (Asp, Glu, Asp) *status predicted F;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) *status predicted
F;40/Binding site: magnesium 2 (Ser) *status pred: F;210,343/Active site: Glu, Lys *status predicted F;245,293,318/Binding site: magnesium 1 (Asp, Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X62667; NID:g50143; PIDN:CAA44540.1; R;Lazar, M.; Lamande, N.; Brosset, S.; Lucas, M.; Keller, A. submitted to the EMBL Data Library, February 1991
A;Reference number: S29675
A;Accession: S29675
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NOMSB
                                                         A;Pathway: gluconeogenesis; glycolysis
C;Superfamily: enclase
C;Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis;
F;40/Binding site: magnesium 2 (Ser) #status predicted
                                                                                                                                                                                                                                                     A; Experimental source: skeletal muscle C; Genetics:
                                                                                                                                                                                                                                                                                     A; molecule type: mRNA
A; Residues: 59-233; (NA', 236-434 <LA2>
A; Cross-references: GB:M20745; NID:g193029; PIDN:AAA37554.1; PID:g387144
                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Lamande, N.; Mazo, A.M.; Lucas, M.; Montartas, D.; Pi
Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989
A;Tille: Murine muscle-specific enorases, CDNA cloning,
R;Reference number: A33921; MUID:89282789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X61600; NID:g50848; PIDN:CAA43797.1; R;Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M. submitted to the EMBL Data Library, October 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-434 <LAM>
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                                                                                                                                                                        A; Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric
                                                                                                                                                                                                        C; Function:
                                                                                                                                                                                                                               A; Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1;
                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A33921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S17109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphopyruvate hydratase (EC 4.2.1.11) beta -
N; Alternate names: enolase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Residues: 1-434 <I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.8%;
100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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        Asp) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and developmental expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gros, F.; Legault-Dema
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Query Match

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Length 434

Query Match

Best Local Similarity

43.8%; 100.0%;

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Length 434

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A; Molecule twrn A24742 A, Mol
                                                                                                                                                                                A;Cross-references: GB:M11931; NID:g204041; PIDN:AAA41119 R;Sakimura, K.; Kushiya, E.; Takahashi, Y.; Suzuki, Y. Gene 60, 103-113, 1987 A;Title: The structure and expression of neuron-specific A;Reference number: PQ0006; MUID:88152493 A;Accession: PQ0006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphopyruvate hydratase (EC 4.2.1.11) gamma - rat N;Alternate names: 2-phospho-glycerate dehydratase; enclase gamma; neuronal C;Species: Rattus norvegicus (Norway rat) C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 22-Jun-1999 C;Accession: A24742; PQ0006
A;Cross-references: GB:M22770;
C;Superfamily: enolase
C;Keywords: carbon-oxygen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; F;40/Binding site: magnesium 2 (Ser) #status predicted F;210,343/Active site: Glu, Lys #status predicted F;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #
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                                                                                                                A; Molecule type: DNA
A; Residues: 1-28 <SA2>
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A; Residues: 1-434 <SAK>
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C; Superfamily: enolase
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A; Residues: 1-434 <SEG>
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A; Title: Enclase isoenzymes i
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   lyase;
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   gluconeogenesis;
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). 3.2;
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Suzuki, Y.
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   glycolysis; hydro-lyase
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                                                                          PIDN:AAA41725.1; PID:g55448
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A;Cross_references: EMBL:X52379; NID:955490; PIDN:CAA36605.1;
A;FBottallCo; L:AT; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas,
Arterioscler. Thromb. 13, 264-275, 1993
A;Title: Cholesteryl ester loading of mouse peritoneal macroph soform.
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S10247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A56781
A;Status: preliminary
A;Status: preliminary
A;Nolectule type: protherin
A;Residues: 'X',60,'X',62-67,'X',69-71;'XX',100-109,'X',111-112,'X',114;'X',184-185,'X'
A;Experimental source: peritoneal macrophages
A;Note: sequence modified after extraction from NCBI backbone
C;Superfamily: enolase
C;Superfamily: enolase; gluconeogenesis; glycolysis; hydro-lyase
B
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                                                                                                                                                         C;Superfamily: enolase
C;Keywords: carbon-oxyc
                                                                                                                                                                                    A; Residues: 1-434 <KAG>
A; Cross_references: EMBL:X52380; NID:955494; PIDN:CAA36606.1;
                                                                                                                                                                                                                          A; Molecule_type:
                                                                                                                                                                                                                                                                                                                                               C;Date:
                                                                                                                                                                                                                                                                                                                                                                          phosphopyruvate hydratase (EC 4.2.1.11) gamma - mou
N;Alternate names: 2-phosphoglycerate dehydratase;
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A;Accession: S10246
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C;Date: 12-Feb-1993 #text_change 22-Jun-1999
C;Accession: S10246; A56781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 18,
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A; Residues: 1-434 < KAG>
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                                                                                                                                                                                                                                                                                                                            ;Species: Mus musculus (house mouse);Date: 12-Feb-1993 #text_change 22-Jun-1999;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999;Accession: S10247
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38, 1990
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                                                                       Mismatches
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                                                                                     A32132
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phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck W;Alternate names: enolase alpha; tau-crystallin C;Species: Anas platyrhynchos (domestic duck) C;Date: 21-May-1990 #sequence_revision 21-May-1990 #C;Accession: A32132
R;Wistow, G.J.; Lietman, T.; Williams, L.A.; Stapel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:119871; OMIM:172430
A; Map position: 1p36-1p36
A; Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; C; Function:
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A;Molecule type: DNA
A;Residues: 1-434 <GIA>
A;Residues: 1-434 <GIA>
A;COSS-references: EMBL:X16288; NID:g31172; PIDN:CAA34360.1; PID:g1167843
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989
A;Note: the nucleotide sequence, R; Croce, C.M.; Showe, L.C.
Proc. Natl. Acad. Sci. U.S.A. 83, R-421-6745, 1986
A;Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human
A;Reference number: A29170; MUID:86313654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: catalyzes the reversible hydration of phosphoenolpyruvate to C;Superfamily: enclase C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; F;2-434/Product: phosphopyruvate hydratase alpha #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X84907; NID:g693932; PIDN:CAA59331.1; PID:g693933 A;Experimental source: endometrium carcinoma cell line HEC-1B R;Miles, L.A.; Dahlberg, C.M.; Plescia, J.; Felez, J.; Kato, K.; Plow, E.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M14328; NID:g182113; PIDN:AAA52387.1; PID:g182114 A;NOte: the authors translated the codon AAG for residue 193 as His R;Walter, M.; Leidenberger, F.A.; Schweppe, K.W.; Berg, H.; Northemann, V. submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: ENO1
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A; Residues: 170-182,'I',184,'R',186-190;245-252 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A39183; MUID:91129243 A;Accession: A39183
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A;Title: Role of cell-surface lysines in plasminogen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-251, 'S', 253-434 <WAL>
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A; Residues: 1-434 <GI2>
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A;Title: Structure of the human gene for alpha-enolase. A;Reference number: S11696; MUID:90323004
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C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Jun-2000 C;Accession: S1196; A29170; S52888; A39183
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N;Alternate names: 2-phosphoglycerate dehydratase; env
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Best Local :
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   L.A.; Stapel, S.O.;
                                                            21-May-1990 #text_change 21-Jul-2000
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Jong, W.W.; Horwitz,

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J. Cell Biol. 107, 2729-2736, 1988
A;Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens struct A;Reference number: A92750; MUID:89079778
A;Accession: A32132
A;Molecule type: mRNA
A;Residues: 1-434 <WIS>
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N;Alternate names: enolase beta; enolase, muscle-specific
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-bec-1989 #sequence_revision 01-bec-1989 #text_C;Accession_633972
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S02072
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                   A; Molecule type: DNA
                                                                                                              A;Cross-references: EMBL:X16504; NID:g31169; PIDN:CAA34513.1; PID:g31170 R;Peshavaria, M.; Day, I.N.M. Biochem. J. 275, 427-433, 1991 A;Title: Molecular structure of the human muscle-specific enolase gene (A;Reference number: S14759; MUID:91222137
                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 **sequence_revision 22-Jan-1993 **text_change 22-Jun-1999
C;Accession: S06756; S14759; S15933; S33330; S08685; S31650
R;Peshavaria, M.; Hinks, L.J.; Day, I.N.M.
Nuclelc Acids Res. 17, 8862, 1989
A;Title: Structure of human muscle (beta) enolase mRNA and protein.deduced A;Reference number: S06756; MUID:90067857
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S06756
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C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Ohshima, Y.; Mitsui, H.; Takayama, FEBS Lett. 242, 425-430, 1989
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A; Residues: 1-434 < A; Cross-references:
                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-434 < PES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphopyruvate hydratase (EC 4.2.1.11) beta - human
N;Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase,
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                                                                       A; Status: nucleic acid sequence
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A; Molecule type: mRNA
A; Residues: 1-84,'A',86-161,'K',163-434 <CAL>
A; Residues: 1-84,'A',86-161,'K',163-434 <CAL>
A; Cross-references: EMBL:X51957; NID:g34788; PIDN:CAA36216.1; PID:g34789
A; Giallongo, A.; Venturella, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feceur. J. Biochem. 214, 367-374, 1993
A; Title: Structural features of the human gene for muscle-specific enolase A; Reference number: S33330; MUID:93292497
A; Accession: S33330
                                                                                                                                                                                                                                                                                                                             A; Experimental source: brain
C; Comment: This is a glycolytic enzyme and murates for tyrosine phosphorylation in Rous saurates for tyrosine phosphorylation in 
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A;Map position: 17pter-17p12
A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Tanaka, M.; Maeda, K.; Nakashima, K.
J. Biochem. 117, 554-559, 1995
A;Title: Chicken alpha-enolase but not beta-enolase has A;Reference number: JC4186; MUID:95355305
A;Accession: JC4186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken N;Alternate names: alpha-2-phospho-D-glycerate hydrolase; eno. C;Species: Gallus gallus (chicken) C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_chan
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A; Residues: 1-434 <TAN>
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Copyright (c) 1993 - 2000 Com
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  1 US-07-973-852-1

US-08-232-538-1

US-08-232-538-6

US-08-232-538-6

US-08-232-538-1

US-08-232-538-1

US-08-874-678-1

3 US-08-643-839-1

US-08-90-151-363-24

US-08-90-111-5

US-08-901-710-5

1 US-08-901-710-5

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1 US-08-901-710-5

1 US-08-91-710-15-1

US-08-91-710-13-1

US-08-643-839-3

US-08-643-839-3

US-08-643-839-3

US-08-645-794-17

US-08-08-653-1913-18

US-08-049-813-18

US-08-08-185-432-17

US-08-08-185-432-17

US-08-185-432-18

US-08-185-432-17
                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (without alignments)
28.735 Million cell updates/sec
                                                                                                                                                                                                                                    Sequence 6, Sequence 1,
                                                                                                                                                                                                                                                                                                                               Description
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| 38 | 38 | 38 | 38 | 38 | 38 | 38.5 | 38.5 | 38.5 | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 39 |
| 42.2 | 42.2 | 42.2 | 42.2 | 42.2 | 42.2 | 42.8 | 42.8 | 42.8 | 43.3 | 43.3 | 43.3 | 43.3 | 43.3 | 43.3 | 43.3 | 43.3 | 43.3 |
| 461 | 461 | 461 | 307 | 45 | 37 | 1394 | 410 | 65 | 1063 | 1063 | 1063 | 992 | 992 | 689 | 689 | 481 | 481 |
| 4 | N | 1 | 4 | N | N | 6 | 6 | σ | Н | Н | \vdash | Н | μ. | 4 | 4 | 0 | - |
| US-08-476-862-2 | US-08-650-000-2 | US-08-385-229-2 | US-09-049-672A-9 | US-08-824-379-3 | US-08-248-839C-65 | 5177197-30 | 5177197-1 | 5177197-51 | US-08-482-847-8 | US-08-127-499A-8 | US-08-093-453B-3 | US-08-482-847-1 | US-08-127-499A-1 | US-09-061-769A-2 | US-09-177-249-2 | 5164481-1 | us-07-927-071-1 |
| Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 9, Appli | Sequence 3, Appli | Sequence 65, Appl | Patent No. 5177197 | Patent No. 5177197 | Patent No. 5177197 | Sequence 8, Appli | Sequence 8, Appli | Sequence 3, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 2, Appli | Sequence 2, Appli | Patent No. 5164481 | Sequence 1, Appli |

ALIGNMENTS

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RESULT 1
US-07-973-852-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Miyazak.
APPLICANT: Motoi, I
APPLICANT: Kodama,
APPLICANT: Maeda,
APPLICANT: Tsujita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/631,321

FILING DATE: 20-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 332884/1989

FILING DATE: 25-DEC-1989

PRIOR APPLICATION NUMBER: JP 75600/1990

APPLICATION NUMBER: JP 75600/1990

FILING DATE: 27-MAR-1990

PRIOR APPLICATION NUMBER: JP 194782/1990

PRIOR APPLICATION NUMBER: JP 194782/1990

PRIOR APPLICATION NUMBER: JP 194782/1990

PRIOR APPLICATION NUMBER: JP 194782/1990
        ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5376640man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 1327-014-0 DI

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500

TELEPAX: (703)866-2347
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: LIPOLYTIC ENZYME INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: V
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1755 Je CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: P.C.

    Application US/07973852
    5376640

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Y: U.S.A.
248855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okuda, Hiromich
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Maeda, Taturo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Motoi, Hirofumi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBLON, SPIVAK, McCLELLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toshiaki
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                                                                                DIV
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US-07-950-773-1
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US-07-950-773-1
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Best Local Similarity
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                                 Matches
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07950773 Patent No. 5411956
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEPAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1/2
STREET: 1/2
CITY: Arlington
STATE: Virginia
*TP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5411956man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                             Local Similarity
nes 7; Conserv
                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/631,321 FILING DATE: 20-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UFILING DATE: 19920924
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & ADDRESSEE: NEUSTADT, P.C.
1 LVVGLCTCQIKTGPAC 16
                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 LCAGVCRCKISSGLSC 39
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                                                                                                                                             AMINO ACID
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                                                                                                                                                            45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1755 Jefferson Davis Highway, Fourth Floor
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsujita, Takahir
Okuda, Hiromichi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyazaki, Toshiyuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maeda, Taturo
                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                    protein
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43.8%;
                                           51.1%;
43.8%;
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                                                                                                                                                                                                                                                                    1327-003-0
                                           Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; D
Pred. No. 3;
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 #1.25
                                                        Length 45;
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                          Gaps
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GENERAL INFORMATION:

APPLICANT: THOMAS, KE
APPLICANT: KENDALL, R
TITLE OF INVENTION: I
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:

CELL GROWTH FACTOR

INHIBITOR OF VASCULAR ENDOTHELIAL

0;

THOMAS, KENNETH A. KENDALL, RICHARD L

CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave

COMPUTER READABLE FORM:

COUNTRY: USA ZIP: 07065-0900

STATE: CITY: Rahway

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В
                                                                                                                                           Query Match
Best Local Similarity
"-+ hes 6; Conserva
                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-232-538-12
                                US-08-786-164-12
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Sequence 12, Appli
Patent No. 5861484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Approx No. 5712380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5712380 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thomas, K
APPLICANT: Kendall,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.III
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                               281 GLYTCRVRSGPS 292
                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/232,538 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rahway
STATE: NJ
                                                                                                                           4 GLCTCQIKTGPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 LCAGVCRCKISSGLSC
                                                                                                                                                                                                                                                                                                                          CENGTH:
                                                                                                                                                                                                                                                                                                         amino acid
               Application US/08786164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08232538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Merck & Co., Inc.
P.O. Box 2000 126 E Lincoln Avenue
                                                                                                                                                                                                                                                                                                                      661 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas, Kenneth A.
Kendall, Richard L.
VENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (908)
                                                                                                                                                                                                                                                                                         single
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                                                                                                                                                                           47.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      35,403
                                                                                                                                                                                                                                                                                                                                                                                                                       18888IA
                                                                                                                                                                           Score 43; DB Pred. No. 89;
                                                                                                                                                            Mismatches
                                                                                                                                                                                          Length 661;
                                                                                                                                                            Indels
                                                                                                                                                            0
                                                                                                                                                          Gaps
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CURRENT APPLICATION DATA:

Microsoft Word 6.0

DOS

OPERATING SYSTEM:

IBM Compatible

Diskette

MEDIUM TYPE:

0,

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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: p
US-08-786-164-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-232-538-6
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Best Local Similarity
Thes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 661 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
            TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 21-JAN-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC COMPANIED STREET
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                        REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 18888IA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Kenneth A.
APPLICANT: Kendall, Richard L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
TITLE OF INVENTION: GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 1888BDA TELECOMMUNICATION INFORMATION: TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 GLYTCRVRSGPS 292
                                                                                               NAME: Wallen, John W.III REGISTRATION NUMBER: 35,
                                                                                                                                                  APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 07065-0907
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                                                                                                                                                                                                                                                                                                                                                                       P.O. Box 2000 126 E Lincoln Avenue
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50.0%;
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Pred. No.
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RESULT 6
US-08-786-164-6
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                                                    Query Match
Best Local S
Matches 6
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                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:

NAME: Mark Hand, J
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1888
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Wo
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APPLICANT: KENDALL, RICHARD L
TITLE OF INVENTION: INIBITOR
TITLE OF INVENTION: CELL GROW
                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 GLYTCRVRSGPS 318
307 GLYTCRVRSGPS 318
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CITY: Rahway
STATE: NJ
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TOPOLOGY: linear
                                                    Local Similarity
les 6; Conserv
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TELEPHONE: 908-594-4720
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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les 6; Conser
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                                                                                                                                                                                TYPE:
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                        GLCTCQIKTGPA 15
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P.O. Box 2000, 126 E. Lincoln Ave.
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                                                     Conservative
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50.0%;
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50.0%;
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INHIBITOR OF VASCULAR ENDOTHELIAL
CELL GROWTH FACTOR
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                                                               Score 43;
Pred. No.
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Pred. No.
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FENGTH: 758 amino acids
                                                                                                                                                                                             Sequence 1,
Patent No. (
                                                                                                                                                                                                                                                                                                                                                                          Matches
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Sequence 1, APP
No. 59521
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APPLICATION NUMBER: US 08/643,839
FILING DATE: 07-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
                                                                   TITLE OF INVENTION:
                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,678
FILING DATE: HEREWITH
                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A-CTELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
TELEPHAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                CORRESPONDENCE ADDRESS:
                                  NUMBER OF SEQUENCES:
                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ferrara, Napoleone TITLE OF INVENTION: NOVEL INH
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CITY: San I
STATE: Cal:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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les 6; Conserv
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 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                               , Application US/08643839
6100071
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                                                          Ferrara, Napoleone
VENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
VENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
                                                                                                                                        Davis-Smyth, T
Chen, Helen H.
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                                                                                                                        Presta, Leonard
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                                                    PRODUCTION
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Hohbach, Test,
                                    48
                                                                                                                                                          Terri L.
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Pred. No. 1e+02;
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Albritton & Herbert
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Best Local
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SEQUENCE CHARACTERISTICS:
                              FILING DATE: 07-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/02906
                                                                                                SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
OPERATING SYSTEM: Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
ARPHICATION NUMBER. IS COM 1643 8:3
                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Segawa, Toshiaki
TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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APPLICATION NUMBER: PCT/
FILING DATE: 07-OCT-1996
APPLICATION NUMBER: 8/21
                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                  CITY: Boston
STATE: MA
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TOPOLOGY: unl
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5. 6270993
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(415) 398-3249
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Okamoto, Masaji
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                                                                                                                                                                                                                                                                                                                                                                                                Niwa, Mikio
                                                                                                               SYSTEM: Windows95
FastSEQ for Windows Version
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                                                                                                                                                IBM Compatible
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                                                                                  us/09/051,363
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Pred. No. 1e+02;
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Gaps

APPLICATION NUMBER: 7/29 FILING DATE: 07-0CT-1995

23-JUL-1996

7/296476 JP

Length 780;

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; TOPOLOGY: lir
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-051-363-24
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14,
                                                                          TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.III
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fraser, Ph.D., J.D., CREETER CELOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
 MOLECULE TYPE:
                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: IN
TITLE OF INVENTION: GR
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thomas, Kenneth A. APPLICANT: Kendall, Richard L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                             FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P.O. CITY: Rahway
                                                 TYPE:
                                                                                                                            TELEPHONE:
               TOPOLOGY:
                           STRANDEDNESS: single
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                             ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $7, Application US/08232538
5712380
                                             amino acid
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GY: linear
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                                                             780 amino acids
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P.O. Box 2000 126 E Lincoln Avenue
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                 linear
protein
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50.0%;
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Pred. No. 1e+02;
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US-08-786-164-14
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                                                                                                                                                                                                                                                                                                   US-08-786-164-14
                                                                                                              RESULT
Sequence 5, Application US/08340011
Patent No. 5776755
GENERAL INFORMATION:
APPLICANT: Alitalo, et al.
TITLE OF INVENTION: FLT4, A NOV
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                      Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Mark Hand, J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 908-594-3905
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MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
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APPLICANT: KENDALL, RICHARD L
TITLE OF INVENTION: INITIBITOR OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: CELL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                          307 GLYTCRVRSGPS 318
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OPERATING JOSEPH SYSTEM
OPERATION DATA: 079/78
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les 6; Conserv
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ZIP: 07065-0900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                      4 GLCTCQIKTGPA 15
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P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                            780 amino acids
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50.0%;
 et al. FLT4, A NOVEL RECEPTOR TYROSIN KINASE 20
                                                                                                                                                                                                                                   47.8%;
50.0%;
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Pred. No. 1e+02;
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Pred. No. 1e+02;
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INFORMATION FOR SEQ ID NO:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         NUMBER OF SEQUENCE CORRESPONDENCE ADDRESS:

CORRESPONDENCE Marshall, O'Toole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
                                                                                                                                                                                                         APPLICANT: Matikainen, Marja-Terttu TITLE OF INVENTION: FLT4, A RECEPTOTITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              APPLICANT:
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APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
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                                                                              COUNTRY: United States of ZIP: 60606-6402
                                                                                                                              STREET: 6300 :
CITY: Chicago
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les 6; Conserv
 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meyers, Thomas C. REGISTRATION NUMBER: 36,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/340,01:
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                                                                                                                                                                                                                                                                                                         Alitalo, Kari
Aprelikova, Olga
Pajusola, Katri
                                                                                                                                                                                                                                                                       Armstrong, Elina
Korhonen, Jaana
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                                                                                                                                                                                                                                                          Kaipainen, Arja
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PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marshall, O'Toole,
00 Sears Tower, 233
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                                                                                               America
                                                                                                                                                                                                                            RECEPTOR TYROSINE KINASE, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                           Gerstein, Murray & South Wacker Drive
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South Wacker Drive
Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1311;
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                                                                                                                                                             Borun
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; MOLECULE TYPE: US-08-901-710-5
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Best Local Similarity
"hes 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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INFORMATION FOR SEQ ID NO:
             APPLICATION NUMBER: US/08/750, FILING DATE: 12-MAY-197 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 1396-
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: APPLICANT:
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPOTER: PC POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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PRIOR APPLICATION NUMBER: 07/959,951
PTILING DATE: 09-0CT-1992
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sharkey, Andrew M.
APPLICANT: Smith, Stephen K.
TITLE OF INVENTION: FLT-15, VARIANTS THEREOF USED AS GROWTH FACTOR INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPEAX: 312/474-0448
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APPLICATION NUMBER: 08/257,754
FILING DATE: 09-JUL-1994
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PRIOR APPLICATION DATA:
08/340,011
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                   411 Hackensack Avenue, 4th Floor
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David A.
7788R: 38,153
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50.0%;
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Pred. No. 1
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1.6e+02;
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; TOPOLOGY: lit; MOLECULE TYPE: ; HYPOTHETICAL: ! US-08-750-141A-3
; MOLECULE TYPE: US-08-874-678-33
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                                                                                    CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/643,839

FILING DATE: 07-MAY-1996

ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-63291-1/WHD

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEFAX: (415) 398-3249

TELEFAX: 910 27729

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1362 amino acids
TYPE: amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 1338 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local (
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Presta, Leonard
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TELEFAX: 201-
TELEX: 133521
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CITY: San Francisco
STATE: California
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                                      STRANDEDNESS:
TOPOLOGY: unl
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                                                                            TYPE: amino acid
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201-343-1684
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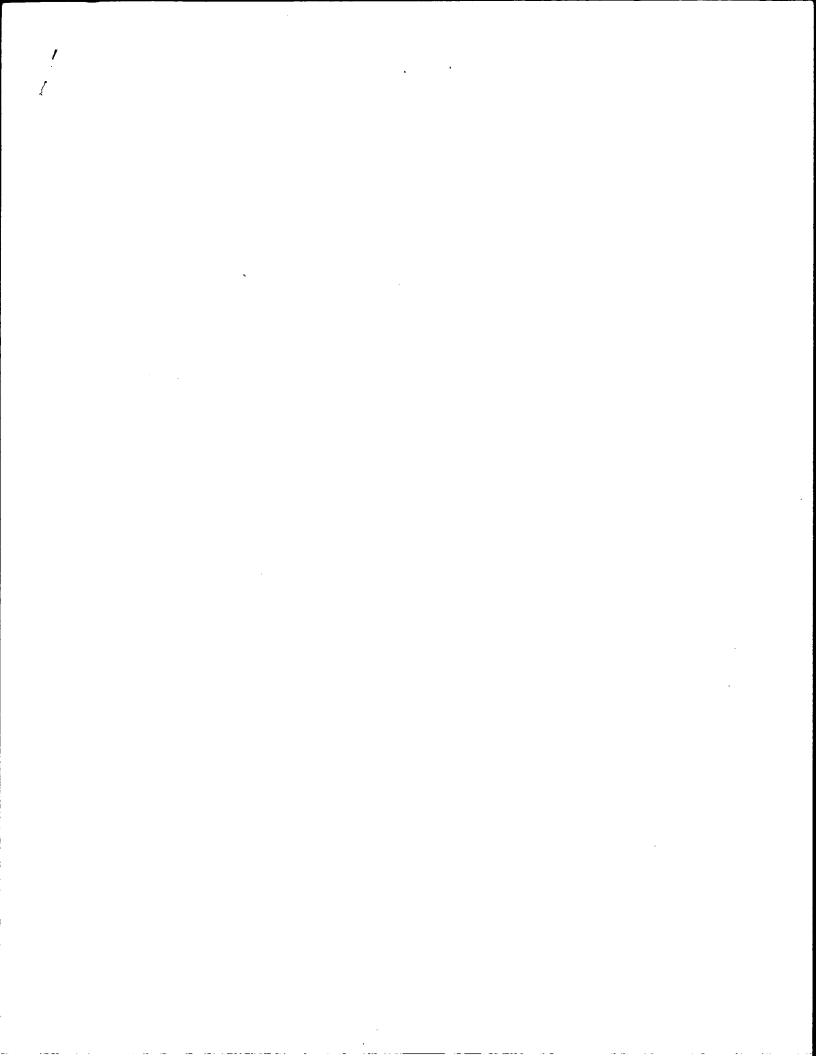
Query Match

47.8%;

Score 43;

DB 2;

Length 1362;



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Title:
Perfect score:
Sequence:
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No.
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Maximum DB seq length: 2000000000
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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    Match
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16
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US-08-763-226C-15
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US-09-307-200-15
US-09-373-685-60
US-09-273-685-60
US-08-513-974B-340
US-08-913-978-52
US-08-913-978-91
US-08-913-918-32
US-08-913-918-32
US-08-913-918-39
US-09-313-31-31
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Sequence 15, Appl
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| RESULT 1 US-08-363-475-3 Sequence 3, A Patent No. 55 Patent No. 55 Patent No. 55 GENERAL INFO GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CORRESPONI ADDRESSE STREET: COUNTRY: COMPUTER: COMPUTER: COMPUTER OPERATIN SOFTWARE CURRENT AR APPLICAT FILING C CLASSIFI ATTORNEY/A NAME: REFERENC TELEFOAN INFORMATION SEQUENCE C LENGTH: TYPE: | 229 230 230 244 240 254 264 276 276 276 276 276 276 276 276 276 276 |
| -3 516679 507MATION: F: Chiang F: Ch | 5 5 3 3 1 |
| Shu-Jen Jr. Willi ean M. PENICILLI FUSARIUM 30 SS: RA. Savits 4000 SS: 1000 SS: 1000 | 369 1 US- 369 4 US- 369 4 US- 389 3 US- 400 1 US- 400 1 US- 400 1 US- 400 4 US- 405 1 US- 423 4 US- 423 4 US- 444 1 US- 444 1 US- 444 1 US- |
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Query Match

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Length

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                                                                                                                                   Sequence 15, Application US/08763226C Patent No. 6057291 GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                APPLICANT: Hancock, Robert E. W.
APPLICANT: Karunaratne, Nedra
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hancock, Robert E. W.
APPLICANT: Karunaratne, Nedra
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/658, FILING DATE: May 31, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460,464
APPLICATION NUMBER: 2, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619/678-5070
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OPERATING SYSTEM:
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           CITY:
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nes 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
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SOFTWARE: FastSEQ for Windows Version 2.0
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4225 Executive Square, Suite 1400
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Best Local Similarity
"heres 5; Conserv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-763-226C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09307200 Patent No. 6297215
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hancock, Robert E. W.
APPLICANT: Karunaratne, Nedra
APPLICANT: Karunaratne, Nedra
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
ATTORNEY_AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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ETLING DATE: 31-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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FILING DATE: 10-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,857
FILING DATE: 31-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
PATA:
                                                                                                                                                                 FILING DATE:
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                                                                                                                                 APPLICATION NUMBER:
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GY: linear
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10-DEC-1996
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                                                                                                                                 08/763,226
                                                                                                                                                                                US/09/307,200
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Pred. No.
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Best Local Similarity
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; Sequence 60, Application US/09273685
            US-09-273-685-60
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                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/00
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alvarez, Vernon L.
                                                                                                                                                                                                                           LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
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STATE: New York
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                                                                                           10 IKTGP 14
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                                                                                                                      Local Similarity les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 NAME: Misrock, S. Leslie
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(212) 869-9741/8864
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100.0%; Pro
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; Pred. No. 33
0; Mismatches
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Pred. No.
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                                                                                                                      Mismatches
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5. 62;
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; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-273-685-60
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GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Bindin
TITLE OF INVENTION: Peptide Librar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6015561
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Alvarez, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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TELEFAX: 66141 F
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                   ZIP: 10036
                                                                                                                 COUNTRY:
                                                                                                                                   STATE:
                                                                                                                                                 ADDRESSEE: Pennie & Lum....
STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen Binding Peptides (Abtides) From Peptide Libraries 103
                                                                                                                                                                                                                                   Antigen Binding Peptides (Abtides)
Peptide Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.2%; Score 5; DB 100.0%; Pred. No. 62
tive 0; Mismatches
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                   Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 43;
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US-08-513-974B-340
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Best Local :
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                               FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                PRIOR APPLICATION DATA:
                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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               APPLICATION NUMBER:
                                                  APPLICATION NUMBER: JP 7-057186 FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 IKTGP 14
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     130 Water Street
                                                                                                                                                                                                                                                                                                                                                                      USA
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(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohtaki, Tetsuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hosoya, Mar
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinuma, Shuji
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20-SEP-1995
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20-JAN-1995
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100.0%; Pred. No
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                  JP 7-007177
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Mismatches
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o. 62;
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Best Local Similarity
"-+-hes 5; Conserv
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; MOLECULE TYPE:
US-08-513-974B-340
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                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                   APPLICANT: Moyle, APPLICANT: Campbe
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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ATTORNEY/AGENT INFORMATION:
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             APPLICATION NUMBER:
                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                 Application US/08425673
                                                                                                                                                                New Jersey
                                                                                                                                                                                                 E: Richard R. Muccino P.O. Box 1267
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11-AUG-1994
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                                                                                                                                                                                                                                                          William R.

11., Robert K.

12. Analogs of Glycoprotein Hormones Having

13. Altered Receptor Binding Specificity and Activity and

14. Michael Receptor Binding Same

15. Michael Receptor Binding Same
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             US/08/425,673
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0; Mismatches
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Matches

FILING DATE: 18-JUN-1991 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA:

PPLICATION NUMBER:

US 07/717,151

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; ANTI-SENSE: US-08-425-673-5
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US-08-907-800A-2
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US-08-907-800A-2
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Best Local (
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APPLICANT: SUN, T
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TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                  TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,961
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SUN, Tung-Tien
TITLE OF INVENTION: METHOD AND VECTOR FOR EXPRESSION AND
TITLE OF INVENTION: ISOLATION OF BIOLOGICALLY ACTIVE MOLECULES IN URINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: po
HYPOTHETICAL: NO
                MOLECULE TYPE:
                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                     TELEPHONE: 202-737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                TOPOLOGY:
                                            STRANDEDNESS:
                                                                                                                                                                                      REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: SUI
                                                                                                                                                                                                    NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                LENGTH:
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                                                            : 184 amino acids amino acid
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              protein
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08-AUG-1997
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US-08-938-534-22
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Best Local Similarity
Matches 5; Conserv
                                Sequence 22, Application US/08938534 Patent No. 5916752 GENERAL INFORMATION:
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                                                                                                                                                                                                                   Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICANT: Gottschling, Daniel E. APPLICANT: Singer, Miriam S.
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TELEFAX: 79-0924
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100.0%; Pred. No.
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o. 2.1e+02;
                                                                                                                                                                                                                                    DB 1; Le . 2.4e+02;
                                                                                                                                                                                                                                                  Length 215;
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CORRESPONDENCE ADDRESS: FITLE OF INVENTION:

Telomerase Compositions and Methods 32

STREET: ADDRESSEE:

P.O. Box 4433

Arnold,

White & Durkee

CURRENT APPLICATION DATA

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

MEDIUM TYPE:

Floppy disk

APPLICATION NUMBER: FILING DATE: 01-JUI

01-JUL-1996

US/08/674,168

Houston

TEXAS

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TOPOLOGY:
US-08-938-534-22
                                                                                                                                                                                                                                                                                                                                                                 US-08-674-168-32
                                                                                                                                                                                                                                                                                                                             Sequence 32, App. 580441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US
FILING DATE: 26-SEP-15
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Parker, David I.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (713) 789-2679
COMPUTER READABLE FORM:
                                                                                                                                                              APPLICANT: SUGIMOTO, MASAKAZU
TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING
TITLE OF INVENTION: ARTIFICIAL TRANSPOSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: SN 08
FILING DATE: October 20,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (/___
TEX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: 77210
                                         ADDRESSEE: OBLON, SPIVAN, FULL STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                 38 IKTGP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 IKTGP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                Application US/08674168
                                                                                                                                                                                                                                              MATSUI, Hiroshi
YOKOZEKI, Kenzo
HIRANO, Seiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                 IZUI, Masako
                                                                                                                                                                                                                                 HAYAKAWA, Atsushi
                                                                                                                                                                                                                                                                                                  MORIYA, Mika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                            OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
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100.08; Pr
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Best Local Similarity
Thes 5; Conserv
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                             INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                          APPLICATION NUMBER: JP 8-325659 FILING DATE: 05-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-810-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 7-166541 FILING DATE: 30-JUN-1995 ATTORNEY/AGENT INFORMATION:
             SEQUENCE CHARACTERISTICS:
                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, TITLE OF INVENTION: METHOD FOR PRODUCING L-LYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 LVVGL 242
                             TELEPHONE: 703-413-2220
                                                                                            NAME: NORMAN F. OBLON REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lir
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                                                                                              24,618
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Pred. No.
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L-LYSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 248;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION UMBER: JP 8-142812
PRIOR APPLICATION NUMBER: JP 8-142812
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24.618
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3000
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-730-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-985-908-11
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US-08-852-730-24
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Search completed: May 8, 2002, 11:47:22 Job time: 113 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08852730 Patent No. 6090597 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.2%; Score 5; DB 3; Le Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                          Query Match

Best Local Similarity

Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCES: 26
CORRESPONDENCE OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 055 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
TIP: 2026
CONDUCTED BEACAGIF FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 LVVGL 242
                                                                                                        238 LVVGL 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LVVGL 5
                                                                                                                                               1 LVVGL 5
                                                                                                                                                                                          31.2%; Score 5; DB ilarity 100.0%; Pred. No. 2. Conservative 0; Mismatches
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lo. 2.7e+02;
                                                                                                                                                                                                                               Length 248;
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